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(54) **SECRETED POLYPEPTIDE
OVEREXPRESSED IN RECTAL TUMOR**

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(75) Inventors: **Audrey Goddard**, San Francisco, CA (US); **Paul J. Godowski**, Hillsborough, CA (US); **J. Christopher Grimaldi**, San Francisco, CA (US); **Austin L. Gurney**, Belmont, CA (US); **William I. Wood**, Hillsborough, CA (US)

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(73) Assignee: **Genentech Inc.**, San Francisco, CA (US)

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See application file for complete search history.

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Primary Examiner—Christine J. Saoud

Assistant Examiner—Jegatheesan Seharaseyon

(74) *Attorney, Agent, or Firm*—Elizabeth M. Barnes; Mark T. Kresnak; Knobbe Martens Olsen Bear LLP

(57) **ABSTRACT**

The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

6 Claims, 168 Drawing Sheets

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FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTTATGCATTG
CTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA
TTAAACAAGGCTGGCCTTGTACTTGGAATACTGAGTTGTTTAGGACTTCTATTGTGGCAAACCTT
CCAGAAAACAACCCTTTTTTGCTGCACATGTAAGTGAGCTGTGCTTACCTTGGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCCAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC
ATCAGTTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWFEQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIIYVRYKQVHALSPEENVIIKLNKAGLV LGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQM QPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSF FGFLLTYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGAATTCTGCTGATCCTGG
TTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAAACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCC
CATTCTCAGCCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGTCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACCTCAGCATCAGGAAGTGAATACTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAAACGGATCCTGTCAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTTGGTCCCAACACATTTCTTTCATTCTTGTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTA
GATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTATAAAACAAACAAAATGCTATGGTAGC
ATTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTG
CCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGV
LNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGD
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDAL EELSRQ
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

Important features:**Signal peptide:**

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
AGAACTCTCCATCCGGACTIONAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
GTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
TCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTTCCATCCAGGT
GTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
AAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAGGACCAAGTTGAAACAGCC
TTGAAAGCTAGCTTTGAACTTGCAGCTATGGCTGGGTGGAGATGGATTTCGTGGTCATCTCTAG
GATTAGCCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTGTCTGATTGGAAGGTTCCAGTGA
GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
ATTATCACCACCAAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAACAGAATTTATTGT
CAGTGACAGTACCTACTCGGTGGCATCCCCTTACTCTACAATACCTGCCCTACTACTACTCCTC
CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATTGATTGTGTGCAGAAAGTTTTTATG
GAAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGCAGCATTCAAGAATGA
AGCTGTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTTGTCTCCTCTTCTTTGGTGCTG
CAGTGGTCTTGGATTTTGCTATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAAT
CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCATA
TGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGC
GATGCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTT
CATGCTCCTTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAGAAGAAAGTCCA
CCCTTGGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT
GCCCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCCT
TTCTAGCCTGGCTATGTCTTAATAATATCCCAGTGGGAGAAAGGAGTTTTGCAAAGTGCAAGGAC
CTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTTG
AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGACCCTTTCTTCA
GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTAAGAGCAAAAGAAT
GGCAGAAAAGTTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC
ACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGAATCACTGTTTAGAACACACACA
CTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCTAGGAAATATACTTTTACAAGTAACA
AAAATAAAAACTCTTATAAATTTCTATTTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
ACTCAGTAATTTGTTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC
AAGTGCTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAAACTAAT
TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT
TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAAGCACATTTTAAAAAGTGCC
ATTAACAAATGTATCACTAGCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATT
TGTGACAAAAAATTAAAGCATTTAGAAAACCT

FIGURE 6

MARCFSLVLLLSIWTTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQFAAYCYN
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFPFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCGCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGGC
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCGGGGCGG
CGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTCAAGCCCGGCCCG
GCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACAACCAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGCTGTGGAGACCA
GCTGTGTGTCTGGGGTCACTGCACCAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGC
ACACCCCTGCCCGTGGAGGGCGAGCTTTGCCATGACCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG
CCAGGAGCTGGAGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTG
CCGCCGTGCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAA
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTA
CATCTTCTTCCAGTAAGTTTCCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGCT
CCCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAACTGCA
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC
TGATTGGTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAAATG
CAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCCAGCAGTGTTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCTCTCTCAGCACAGCCTGGGG
AGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACACAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACCTAATTCTCACATCCCTCTAAAAGTAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACTGCAGAAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTCAGGTGTCATGGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEAAAKASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRM LCTRDSECCGDQLCVWGHC
TKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLDLITWELEPDG
ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVRQEELEDLE
RSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG
GCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCCTT
AACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAGATAGCCCGGGTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCTTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAAAATGCGTTTCATGCTACTCATGCGAAAC
ATTGTCAGGGTGGTTCGTCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGTCTGTCTTCTTTTTTTCTCCGGTCGCATCCCGGGCTGGGTAAAG
ACTTTAAGAGCCCCCACCTCAACTATTACTGGCTGCCCATCATGACCTCCATCCTGGGGGCTAT
GTCATCGCCAGCGGCTTCTTCAGCGTTTTTCGGCATGTGTGTGGACACGCTCTTCCTCTGCTTCCT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGA
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA
AAGATTTTATTAAAGATATTTTGTTAACCTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLFWTL
NWVLALGQCVLGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
IVRVVVLDKVTDLLLFFGKLLVVGGVGVLSEFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC
TCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCCGC
CAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCTCTTCTGCGGGTGCTGGTGTCCA
TCATTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGCC
GGGATCCCCACCGTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
CATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTTACCCTGCTCATGCTCTGCGTGAGCAGCA
GCGGGGACCCCCGGGCTGCCATCCAGAATGGGTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTC
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGCGCTCGTGGG
CTCCTTCTCTTCATCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGT
GGCTGGGCAAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTC
TTCTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCCAGCGGCTGCCA
CGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGTGCTGTCTGCG
CCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTATCACCCCTCTACACCATG
TTTGTCACTTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCATTTGCCAACCCAGCT
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCCGAGCATTG
TGGGCCTCATCATCTTCTCCTGTGCACCCCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
AACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGAGGT
GGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCC
ACTTCTGCCTGGTGTGCTGGCCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCCGGTGAG
ACCCGGAAGATGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
CCTCTACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCTCA
CAGCCTGCCATCTGGTGCCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
CCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCCCTGAGCCGGGC
CTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
ACCCACACGGTGGAGCTGCCTCTTCCCTCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA
AGGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCACACAG
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCTCTG
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 12

MGACLGACSLSCASCLCGSAPCILSCCPASRNSTVSRLI FTFFLFLGVLSIIMLSPGVESQL
YKLPWVCEEAGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQRWLGAKE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVITYSY
SFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVWKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCCGTTAAGGTGTCTTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTTGTACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTCATC
CTTGCCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTTATACCTGGTGGTCTTTTCTGATG
GTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTAAATGTGAAAAACCCCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGCAGTGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTTATTGAACAGCTAATAAAGATTTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAGAAAGTCTTGTGCTGTATTCCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCATTCAC
AGAATGGAATTTTTTTGTTTCATGTCTCAGATTTATTTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTTAACTCATGCACATGTGCTCTTTGTACAGTTTTAAAAAGTGTAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTT
TTATCATGAAATCATGTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGC
ACAAAATGACTTAAACCATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRFTCLFVTFDLLF
VTLLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGACTGAGG
CCGCGGCCTGCCCCGCGCGGCTCCCTGCGCCGCGCGCCTCCCGGGACAGAAGATGTGCTCCAG
GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAAGGGCTGCCCAT
CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCC
CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
AGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCC
TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
CATGAAATCACC AATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA
CCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGCTCGACCGCCTCCTGGAGCTCAAGCTGC
AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGC
CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT
GGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACG
CGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGC
TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC
TCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGC
TGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCA
CTTCCCGCCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCCAG
CCACCACCACCACAGCCACAGTGCCACCACGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCT
TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTC
CACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACG
GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTACGCGCGAG
GCCACCACGGTCCCTGACCCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGC
AGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
GGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCAACCA
GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAGG
GCGAGGAGGCCTGCGGGGAGGCCCATAACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCAAC
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
GCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG
ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAACCTGGAGGGAGTGAAGGTCCCTTTGGAG
CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
ACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCCTCCACGCAAAGCCCTACATCTAAGCCA
GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
ACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
GGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
CTAACGTCCCCAGAACCGAGTGCCATATGAGGACAGTGTCGCCCCCTGCCCTCCGCAACGTGCAGTC
CCTGGGCACGGCGGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC
TCCAGGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC
GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGC
TTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCT
GGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAA
GGCCTTTTGTAAAGAAAAATAAAAGATGAAGTGTGAAA

FIGURE 16

MCSRVP L L L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q G T R P S P T P
V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y
T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E G V K V P L E P G P K A T E G G G E A L P S G S E
C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

[illegible]

FIGURE 18

MRVRIGLTLLLCVLLSLASASSDEEGSQDES L DSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPPFLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEEAAKRRQMQEAMMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFEEKLTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTFGALGGNLIAHMLVLSRL

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAGCCCATTCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAATAAGATTGAAGACATCACTG
ATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACTTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTGGTGT
CCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAAA
AGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGNKSYVNMD
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAE LANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCATCGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAA
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
CATTCAGAAATATATTCCATGCTATCAGCTTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATTCGGT
CGTCATTCAAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAACTTGCAGGAGCATTT
TTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
ATCGACTGGAACATTTCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTT
GCCAATCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCCCTGTATGTCCACTGG
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTTGAAGAAGATGGATCCTTAAAGGAGG
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTG
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA
GAAAAGGAGAGGAGCACAGATTCAAGCAGCAAGAGAGAAGAACATCCAAAAAGACCTCAGGAGA
ACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATTCCTGAATTCCTTCATTCATGTGTT
ATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACCTCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAC
AAATCATTAAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTA
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
CTACATTTTTGATCCTTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAAC
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTCAAC
TGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAACATCA
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCTTACACAG
ACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
GAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTATTTTCAAATATGGAAA
GAAATTTATATGAAAATTTATCTGAGTCATTAAAATTCCTTAAGTGATACTTTTTTAGAAGTA
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
AAAATTTAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSSRAV
QTHSSKFFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL
MVEHTDIPEASPASTPQIIKHKALDLDDRWQFKRSRLLDTDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTF

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCCCAA
GCAGCGCGCAGCGAACGCCCCCGCCGCCACACCTCTGCGGTCCCCGCGGCGCCTGCCACCTTCCCTCCTTCCCC
GCGTCCCCGCTCGCCGCGCAGTCAGCTTGCCGGTTGCGTGCCCCGCGAAACCCGAGGTACCAGCCCGCGCCTCT
GCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGCGCCTGGCACCGGGACCGTTGCCTGA
CGCGAGGGCCAGCTCTACTTTTCGCCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACTCCAACCTCTTCCC
TCCAGCTCCAACGCTAGTCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCGCTTCCCGTCCGGTCCCAA
GGTGGGAACGCGTCCGCCCCGCGCCGACCAATGGCACGGTTGCGCTTGCCCGCGCTTCTCTGCACCTGGCAGTGCTC
AGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGACGTCTTACGTGTCAAAGGCTTC
AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCCAGGGTTCTACCTGTGCTCT
CAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTG
CAAGCTGTCTTTGCTTCACGTTACAAGAAGTTTGATGAATCTTCAAAGAATACTTGAAAATGCAGAGAAATCCCTG
AATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAAAATTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTG
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATG
TTCGCGCTGGTGAACCTCCAGTACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
CCCTTCGGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTGCTCAAGGC
TTAGCGGTTGCGGGAGATGTGTCGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGATACCCATGCCCTGTTGAAG
ATGATCTACTGCTCCCACTGCCGGGTCTCGTGAAGTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGC
TGTTTGGCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
GAGGGTCCCTTTCAACATTGAATCGGTTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAAGAT
AATAGTGTTCAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
TCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCGAGGAACGCCCAACCACAGCAGCTGGCACT
AGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCTCCCTTCGAGCAAC
GTTTGCAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
CTGTTTGCACTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACCAGAC
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA
CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCTGGTTATGCAGAGAGAGTGGAGATTAATTCTCAAACCTCTGAG
AAAAAGTGTTCATCAAAAAGTTAAAAGGCACAGTTATCACTTTTCTACCATCCTAGTGACTTTTGCTTTTAAATGAA
TGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGCTGACTTTGTTTCTCATTCAGTTTTGGG
AGGAAAAGGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
CTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTGTTTGTATGTTTCTCATTTCTGTTTGTGGGTT
TTTTTTTCAAACGTGATCTCGCCTGTTTCTTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATT
TCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATCTTATTAAAAGAAAAGCCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGST
CCSQEMEELKYSLOSKDDFKSVVSEQCNHLQAVFASRYKKFDEFKELLENAEKSLNDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGNVNLEMLNDFWARLLERMFRLVNSQYHFTDEYLECVSKYTE
QLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
VTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSLPSNVCNDERMAAGNGNEDDCWNGKKGKSRYLEAVTGNGLANQGNNPEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:**Signal peptide:**

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTCCTGAG
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACCTCACTCTCCCAGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGTTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT
AGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTT
AAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISLLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM .
TVSGLPKKQCPCDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGCTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTG
CTCTGTGCAGAGCCCCAAGGAAGGTCCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTC
GAGCCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA
GCAGAATGAGAGAAGACATTTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTC
CCAATGTTGTCCCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTPLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSSQIKGL
TGASGKVALLELGCCTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM
RQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLEFFWEHVAEPYGSWAFMWQQVFEPW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHEMKGAVKQSFSSKALICSFPSL
QLEQATHQPIYLPLRGT

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCCTATCCACCTCCCCAAGCCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTCAATTAAGAAATT
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGGAATCATGTCGG
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
TTCAGATTTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTATTTTGGGATTGTTGTT
TGCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
AAATAAAGCCATCAGCAGTGCTCCCTTCCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACTGCAGGAGCTGCCCAGGTT
ATGGAAGGCGGCCAAGTGGAATATAAGCCCCCTTCGGGCATTCCGGTACATGTGGTCGTACCATTT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
TGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATCATCCCATCCTTTCTGCTCTC
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG
GATTCCGAGAATCATTGTCATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
ATTCAAAATCTTGTTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
TTTTTCTAGGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTTGGAGGACTCATGGCTTTTAACTAC
AATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC
TGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
TTAAAAGACCTAATAAACCTATTCTTCCCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDLSIE
LDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTF
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQTIA
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQLALKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVVHSLVSVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

Important features:**Signal peptide:**

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 33

[illegible]

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR
ESFIVLESKPKKGVTPSALTYSSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA
TPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQRQDPSGAAFQKP
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPATHFNLKTHTN SRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENЕКQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTLLQPLVKRVCDTDR LACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISD TDTRIGAVQYTYEQRL EFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG VITYAIGVAWAAQEELEVIATHPARDH SFF
VDEFDNLHQYVPRIIQNICTEFN SQPRN

Important features:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633**Amidation site.**

amino acids 304-308

FIGURE 35

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGC
CAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAAT
ACAGAAAACAACAAAAAACTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCC
GGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCCGAGTGTA
AAGAACCCTTCGGCTCGCGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTA
GGATGTCACTGAGATCCCTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTAC
CTCAGCCTTCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTA
CAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTTCTGGTCATTC
TGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCT
TGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGC
ATTGTCCTTAGAGGATGAACACCTTCTTTATGGTGACATAATCCGACAAGATTTTTTAGACACATATAATA
ACCTGACCTTGAAAACCATTTATGGCATTTCAGGTGGGTAACTGAGTTTGGCCCAATGCCAAGTACGTAATG
AAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGA
GAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAAACCCATATTT
CTTACCAGGAGTATCCTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTATATAATGTCCAGAGAT
TTGGTGCCAAGGATCTATGAAATGATGGGTACGTAAAACCCATCAAGTTTGAAGATGTTTATGTCCGGAT
CTGTTTGAATTTATTAAAAAGTGAACATTCATATTCAGAAGACACAAATCTTTTCTTTCTATATAGAATCC
ATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTT
TGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACCTCACATTCTACAAAAAGCCTAGAAGGACAG
GATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTT
ACACTGAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG
CCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGG
ACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGGTGTTACTGAGTTATAAGCTCA
CTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTA
TATCTTATGTGGATTACCAATTTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATA
CTGAACAAAATTTTACCTGTTTTTGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATT
ATTATTTAAATTACTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAG
TGAATCATTCCTTACATGCAAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCACTCCA
TTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTTAAATATTTTACTGTGGT
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLL
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:**Type II transmembrane domain:**

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGGACCAGCCGCGGCAAGGATGAGAGCTGGGTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATG
TCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATGTGTGCGGGAGTGTGTG
AATATGATCAGATTGAGTGGCTCTGCCCGGAAAGAGGGAAGTCGTGGGTATACCATCCCTTGTGTCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAAACTGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT
ACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGTCATGCGATGTG
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGTGAAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTTCATGT
TAAACCTGGGTTTGTTCATCCAATAAGATTGTGTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATEACTATGTTGAG
GTTCTGTATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAG
GATCCTCACTCCACGTCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGC
ATGCTCCTCATCCCCTTGTTTCCATGACGGCAGCTGCGCTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC
TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCTGGGGGGCCAGTCAATGGGTACCAGAAAA
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAAATTGGCACCGTGGTGTCTTTCTTTTGTAAACAATCCTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGGAACAGCCCATCTGCATAAAAGCCTGCCGA
GAACCAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCCGATGCAGGTTCACTCAAGGGAGACACCATTACACCAGCTAT
ACTCAGCGGCCTTCAGCAAGCAGAACTGCAGAGTGCCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGG
ATACCAACATCTGCATACCAGCTCCAGTATGAGTGCATCTCACCCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGT
CTGAGGACTGGGAAGTGGAGTGGCGGGGCACCATCCTGCATCCCATCTGCGGGAAAATTGAGAACATCACTGCTCCAAGAC
CCCAAGGGTTGCGCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGC
GTGGTTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCCACTGTGTTACTGACCTGGGGAAG
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATTCTACCGGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATTCTGCATCCCACTATGACCCCATCTGCTTGATGCTGACATGCCATCCTGAAGCT
CCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCACTTCTTCCAGGAG
TCCCACATCACTGTGGCTGGCTGGAATGTCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCCACTGAGTGTCTACTGATAACATGTT
CTGTGCCAGCTGGGAACCACTGCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGTCTTCCGGGA
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCA
CTGCCCTTACCAAGGTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG
TGTTTCTGTATATCCGCTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCCCTGTGAACCTTGGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAGAAGACCATATACAAAACCTTCCA
CTCCACTGACCTGGTGGCTTCCCCAACTTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCCTTTGGAGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCT
TGTGTACATGGCCACAGTACAGTCTGGTCTCTTCTTCCCTTCCCCATCTCTTGTACACATTTTAATAAAAAAAGGGTTGGCTTCT
GAACTACAAAAA
AAAAA
AAAAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII
KRVCGNERPAPIQSIGSSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNSYVLSGNE
KRTCQONGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLYSAAFSKQKLQSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVVSVDSSLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLVSVSYDKTCSHRLSTAFTKVLFPKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTATTAAACGTGGCTTAATC
TGAAGGTTCTCAGTCAAATTTCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGCTTCTGTTGC
TGGTCTTGCCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATTGAGAACTCTGTA
AAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA
ACCCTGCCTACGFGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA
GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA
GGACAAAGAGCGGGAGTGCAAGTTGCCAACCATGCCGACCAGGGCAGGGAAAAATTCTGAAAAACCACTGCCCTGAAG
TCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCATCAAGATCAATCGAGTAGATCCCAGTGAAA
GCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCACTGGTCCATATCATTATCCAACACATTTATCGTGATGGGG
TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTC
ACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCA
GCAGGAACAATGGACAGGCCCGGATGCCTACAGACCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCC
CCGAGGAGCAGCTTGAATAAACTGGTGCAGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCG
GTGTGGCATATCGACATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCA
GCCCAGAAAGTGCGGCTCATCTGATTACGGCCAGTGAAAGACGTGTTACCTCGTCGTGTCCCGCCAGGTTCCGCGAGC
GGAGCCCTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCAGGGCCAGGGGAGAGGAGCAACA
CTCCCCAAGCCCTCCATCCTACAATTACTTGTCTATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCG
GCATGACCGTCGAGGGGGAGCATCACATAGAGAATGGGATTTGCCATCTATGTCATCAGTGTTGAGCCCCGAGGAG
TCATAAGCAGAGATGGAAGAATAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC
GGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAAGTCAAAGAGTATGAGC
CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCT
GGGTGATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
TGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAACAAACCTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAATGA
TACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTGGCACTT
TTTTATAGAAATCAATGATGGGTGAGGAAAACAGAAAAATCACAATAGGCTAAGAAGTTGAAACACTATATTATC
TTGTGAGTTTTTATATTTAAAGAAAGAATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
ACACCTCAGAAAATATGATTCCAAAAAATTAAGCTACTAGTTTTTTTTTCAGTGTGGAGATTTCTCATTACTCTAC
AACATTGTTTATATTTTTCTATTCAATAAAAAGCCCTAAACAACATAAATGATTGATTGTATACCCCACTGAATT
CAAGCTGATTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTTAATTTACAGCT
AAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPS
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINR
ALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSSELSIRLV
GGSETPLVHIIQHIYRDGVIARDGRLLPGDIIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGVFI FNVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQSPDIFQEAGWNSNGSWSPG
PGRSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPYVISVEPGGVISRDGR
IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
CTTGCCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
TTCCACCTTTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGC
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCCATAAGCAAAGGAGTTCATGGCTAATTTCC
ATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTT
GACAACTGTCCTTCTGTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
TTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
CATCTGCATCCCTTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
TAAAAAGTTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
ACTGCTTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
CATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGG
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACACTACTGGGGAT
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
CCTGAAGTGGGTAAATATAACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAAT
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCC
TGGATCTTTTGGTGATGTTTGGAGAAGTGAATCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAA
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTCT
TAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGAT
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
AGGTACGAAGATACAATACTGTTATTCAATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGCAGGT
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTTGGGAATGAAGA
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
CTTCAGGGGAGGACCTGCCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
TTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLT FHL SYKFRLLLLLTLC LTVVGWATS NYFVGAIQEIPKAKEFMANFHKTLLILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNGFSNNYWGWWGGED
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 43

[illegible]

FIGURE 44

MALSSQIWAACLLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

FIGURE 45

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCCTG
GACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG
GTCCTCCTGTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTTAGACAGCAGTGCCTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCACTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTATAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTTGGGCT
CAGTCAGATAGTCATCGGTTTCCTTGGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNANCEFSL
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMA SGWRASSFHFDSEENKHRLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT
TTCTGATCAGGAGGCTTCTTTATGAATTAACTCGCCCCACCACCCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS
SQKQHSPVPEKAIPILITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

[illegible]

FIGURE 52

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNI GEALGHGLGDALSEG VGKAIGKEAGGAAGSKVS
EALGQGTREAVGTGVRQVPGF GAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGV
GHSGAWETSGGHGIFGSQGGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNF
GTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSSGGS
SSGSSSSGSSSGSSGGSSGGSSGNSGGSRGDSGSESSWGSSTGSSSGNHGGSGGGNGHKPGCEKPGNE
ARGSGESGIQGFRGQGVSSNMREISKEGNRLGSGSDNYRGQGSWSGSGGDAVGGVNTVNSETSPGM
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 53

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGG
CTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCT
ACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACCTGCCGCCGGCTCCAGTGTTTCC
CACAGCCCCCAAAACGGAACTGGTTTTTGGGGTCACCTGGGCCTGATCACTCCTACAGAGGAGGGC
TTGAAGGACTCGACCCAGATGTCCGGCCACCTATTCCCAGGGCTTTACGGTATGGCTGGGTCCCAT
CATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCAATGCCTCAGCTGCCA
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATACTGCTG
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCCCCTTCCATTTCAACATCCT
GAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGG
CCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTA
CAGAAATGCATCTTCAGCTTTGACAGCCATTGTGAGGAGAGGCCAGTGAATATATTGCCACCAT
CTTGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCCAGCATATCCTCCAGCACATGGACTTTCTGT
ATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCTGGTGATGACTTCACAGAC
GCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAA
AGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCAG
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCG
ACAGGAGGTGCAAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCC
AGCTGCCCTTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATC
TCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTG
CCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGACC
CCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCCTTTCTCCGCA
GGGCCCAGGAACTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGGCGTTGAT
GCTGCTGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGC
GCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCCTGAATGTAGGCTTGCATGACTTTCTGAC
CCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFFQPPKRNWFWGHLG
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGEGILLSGGDKWSRHRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDShCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLLSKDEDGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

[illegible]

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

[illegible]

FIGURE 58

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIKLSVFIPSQEFSTYRQWKQKIVQAGDKDLG
QLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILKSMDKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGG
AGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMALRKTGQYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCT
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCTGATAT
CGTGATAACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
AGCTGTGCGGAGCAGGATGAAATGTTTCAGAGGCCCGACAGCAGTGTGCTGATCAAGTGATAGTT
GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATAC
CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGA
TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
ACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
CTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
GTGCCTTGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGA
GTGATAAGTAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
CACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGC
TGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCAC
AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTC
TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6o

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC
YIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVSVLYNVTINNTYSCMIENDIAKATGDIKVTESI KRRSHLQLLNSKASL
CVSSFFAISWALLPLSPYLMLK

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
GGGCTACCCCCCTGGTGGTGGTTATGGGGGTCTGCCCCCTGGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCCTCTGGAACCTCAGGAGGACCATATG
GCGGTGCAGCTCCCGSGGGCCCCCTATGGTCAGCCACCTCCAAGTTCCTACGGTGCCCAGCAGCCT
GGGCTTTATGGACAGSGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCTCTT
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCCAGTTCACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGCACCAGGGACCTT
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCTGCATCATAGCCACCA
AATAGTGAGGACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCCCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAATGG
AGTTAGTGTCCAGTCAGCTGAGCTCCACCCTGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCAAAGTGGAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCTGCCACACCCATAAAT
CCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDS DH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNL FQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

[illegible]

FIGURE 64

MQGRVAGSCAPLGILLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSSTGPSNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMAAAAEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRRLPRSNSLGAGGKILSQRP
PWSLIHRVLPDHPWGTLNPSVSWGGGGPGTGWGTRPMHPHEGIWGINNQPPGTSGWNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPPGVLRRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCCTC
CTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 66

MGSGPLVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTCGCAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGACGGGCT
GCCTGCCCATCTAGGTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCCTGAGGTCAAGAGAGGATGGGGCTATTCACTTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVVFS
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

[illegible]

FIGURE 70

MGLFRGFVFLVLCLLHQSNTSFIKLNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFE
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMEMQSIDSVVEFCNEKTHNQEAP
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTTPPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR
MNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPITYPLGGTSICSGIK
YAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPSPISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNQGVYSRYFTAYTENGRYSLKVRAGGANTARLKLRLPLNRAAYIPGWVNGEIEANPP
RPEIDEDTQTTLDFSRASGGAFVVSQVPSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDN
FDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVI
VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGGAAACCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGCAGGGGTGA
CAACAGGTGTCATCTTTTTGATCTCGTGTGTGGCTGCCTTCCTATTTCAAGGAAAGACGCCAAGSTAATTTTGACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTTGGTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCA
GTGCTCAGAAGTGACTTGCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCCTCTTGCTGTTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCTTTAAA
AGTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGCCCGGCTTTGAGGGATGCC
ACCGGTTCTGACGCATGGCTGATTCTGAATGATGATGGTTCCGCCGGGGCTGCTTGCCTGGATTTCGCCGGTGTG
GTTTTGCTGGTGTCTCTGCTGTGCTATCTCTGTCTGTACATGTTGGCTGCACCCCAAAGGTGACGAGGAGCAG
CTGGCACTGCCAGGGGCCAACAGCCCCACGGGGAAGGAGGGGTACCAGGCCCTCCTTCAGGAGTGGGAGGAGCAGCAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG
AATGGGCAGTACCAAGCCAGCGATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC
CTGGCCTTCCGTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG
CCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCGAGGAGAAGCCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGAAGCCATTGAATCAGCCTTGGAGACCTGAACAATCCTGCAGAGAACAGC
CCCAATCACCGTCTTACACGGCCTCTGATTTCAATAGAAGGGATCTACCGAACAGAAAGGGACAAAGGGACATTGTAT
GAGCTCACCTTCAAAGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTCGACCATTGAGCCCCATCATGAAA
GTGAAATGAAAAGCTCAACATGGCCAACACGCTTATCAATGTTATCGTGCTCTAGCAAAAAGGGTGGACAAGTTT
CGGCAGTTCATGCAGAAATTCAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAAGCTGCCAATTCAGGAACTTTACCTTCATC
CAGCTGAATGGAGAATTTTCTCGGGGAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGAAGCAAGCTCCTTCTC
TTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAG
GTATTTTATCCAGTTCTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCACTCCCTCCCTTGGAG
CAGCAGCTGGTCATAAAGAAGGAAACTGGATTTTGGAGAGACTTTGGATTGGGATGACGTGTGAGTATCGGTTCAGAC
TTCAATCAATATAGGTGGGTTTGATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGGACAGTACAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGCGCCAGCTGGGCATGCTG
GTGTTTCAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAAAGACAAGTAGCAAAAAACATGAACCTCCAGA
GAAGGATTGTGGGAGACACTTTTCTTCTTTTGGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAA
GGACGACAAAAGAATTGGACTGATGGTTCAGAGATGAGAAAGCCTCCGATTTCTCTGTGTTGGGCTTTTACACAGA
AATCAAATCTCCGCTTTCCTGCAAAAGTAACCCAGTTGCACCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGGTGTGGAGGTTTGTGATGGTGTTACAATACACTGAGACCTGTTGTTTGTGTGCTCATTGA
AATATTCAATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGATAGGCTTATTATGATACT
AGTGAGTACATTAAAGTAAAATAAAATGGACCAGAAAAGAAAAGAACCATAAATATCGTGTCAATATTTCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTGGTTGTCTTTTAACTGTCTCCGTTTTTTCTTTTATTTAAAAATGCAC
TTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCACTTTGCAAGCCTTACAAGAGAGCACAAAGTTGGCCTAC
ATTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCAAGTTCAAAGCATCAAATGATGCCATAT
CCAAGGACATGCCAATGCTGATTCTGTCAGGCCTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTTGTACT
AATACAGACGTACAGATACTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC
ACTTCTGCTTTACAGAAAAGGAACTCATTGAGCTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCACATTTT
CTCCTCAGAAGTAGGGACCGCTTCTTACCTGTTTAAATAAACCAAAGTATACCGTGTGAACCAACAATCTCTTTT
AAAACAGGGTGTCTCCTCGCTTCTGCTTCCATAGAAGAAATGGAGAAAATATATATATATATATATATATATATGT
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTGCTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACCTGAATATTTTTTAAATTAAGCAGTTCTACTCAATCACCAGATGCTTCTGAAAATTGCATTTTATACCATTT
CAAATATTTTTTAAAAATAAATACAGTTAAATAGAGTGGTTTTCTTCAATCATGTGAAAATATTAGCCAGCACCAG
ATGCATGAGCTAATATCTCTTTGAGTCTTGTCTTCTGTTTGGCTCACAGTAAACTCATTGTTTAAAGCTTCAAGAAC
ATTCAAGCTGTTGGTGTGTAAAAAATGCATTGTATTGATTTGACTGGTAGTTATGAAATTTAATTAACACAGG
CCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEW
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGOYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAN
TLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANERNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLF
SQQY NPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYR
KYLHSNLIVVRTPVRLFWHEKRCMDLTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHL
RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

FIGURE 73

[illegible]

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQ
PHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQINSEAT
FAELHIVHYSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLGTLFSTEEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCCLLLAVYFIARKIRKKRLNRKS
VVETSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGCGCCTTGGGGACGGGCAGTTCCTGTGTC
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCTTTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGGCCTGAAGAGCAGGA
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA
TCCCCAAACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGTTATA
TGTGCAGATGGAAAACTGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTGAGTGT
CTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGTTGTTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAAATTTATTCAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKH PANLILYIGNEFDKRFFVPAEK
IVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTT DICAGPEEQELSLQEEVSTQGTLLESQA
ALAVLGPQTLQYSYTPQLQDL DPLAQEHTDSEEGPEEE PSTTLVDWDPQTGRLCIPSLSSFDQDS
EGCEPSEGDGLGEEGLLSRLYEFPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCGAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
CTGGGAAGATGGCCCGCCCGTGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
CAAGCCACCCTCAGTCCCCTGCACTGAGTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC
ATCTGGCTGAAGGTTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA
TCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
CCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTA
TAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGCAGGTTCATGAACCTCCTAGTGCCATCCCTGC
CCAATCTAGTGAAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
CTCCTGCAGCTGGTGAAGGTGCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTA
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCCACCCTGGACAACATCCCG
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTT
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAACATCATCACTGAGATCATCCA
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTGATTGGTGAAGG
CCTTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCC
TTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG
GTCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
CCTGTGAAAAA

FIGURE 78

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIEKLTQELKDHNATSILQQLPLLSAMREK
PAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSQVPVSLVKALG
FEAAESSLTKDALVLTASLWKPSSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCCTTCTGGGCCTGCCCCTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTC
ATTCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCCTACAGCCTGACAGGGTATGTGTGAAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTAAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVG YILG LLLG LTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNSSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCT
GCCCACCGCTGCTTCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
GTTGATCTGTGGCCCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
ACCAGCGCCTGACCCTGGGGAAAGGATGGTTCCCCGAGGTGAGGGTCCTCTCCTCCTTGCTGGGA
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCCGCCAGACATGTTCTGCCTTTT
CCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
GTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
TCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCCAGCACAAACGGGACCATGTACCAACACGGAG
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAGTGTGTCTCTGCAGCTGC
ACAGAGGGCCAGATCTACTGCGGCCTCACAACTGCCCGAACCAGGCTGCCAGCACCCCTCCC
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACA
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAG
AGAGGCCCCGGGCACCCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT
GTGTGCATGGCGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCCAGAGG
ACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC
CTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGGC
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGAATCAGATCAAGAAAGTCAG
GAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAGGAAGGTCACT
GGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAG
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELF
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPSTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKACVHGGKTYS
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKVKAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVFGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPARRSLERLPSPDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTCTAATCCATCCGTCACCTCTCCTGTCA
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAG
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCACTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTCTAGCACTGGGCTCAGTTCCCTCTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTCTAGTCCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTGTCC
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
GAGATACCTTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATAATCCAGGCGGAACCTGGACTG
GAGAAGAAAGCACGACAGGCAGAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAG
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA
CTGGGAGGTGGACGAGGACACAATAAAAGGTGGCGCTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT
ACATTAAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTCTGGACTA
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGGTTTTG
AAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGCAATCCCAGAGACAAGCAACAG
TGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCA
GATGAAGGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAG
AACCGTCAGGAATCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGTATCCTAATGTTTGTTCATTATATTACACTTTTCAGTAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCLSPKTNAEAMEVRFFRGQFSSVVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPQGDLSTDSRTNRMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAQEVPHSEKRF
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPRTPTPKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTSNESSSQATTPLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCCCCCT
GCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
GGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
TACTTCTTTCTGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACCCTGGAGTCCGGCTGCCCCC
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
GGGACCTCCGTGTCCCCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCTCATCCCACA
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA
ACAAGACCGTCCATCTCAACGTGTCTTACCCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGA
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCT
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGA
GAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCT
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAG
CCACAGCCCTGGTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCCTGCAGGAAGAAA
TCGGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTC
AGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAG
CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCCAGGCAAGGGAGAAGTCA
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCC
TCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVSPLDPSTTRS
SVLTLIPQPQDHGTSLTQCQVTFPGASVTTNKTVHLNVSYPQNLTMTVFQGDGTVSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLNVSLSKATSGVTQGVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGTGIE
DANAVRGSSASQGPLEPWAEDSPPDQPPASARSSVGEGLQYASLSFQMKPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCTAT
GGCCAGCGGGAATTCAGTGCGGGATTTGTTCA GTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTTCTGGTTTTGATTGGAGTGGATAT
GGAACATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAAA

FIGURE 88

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVI PVVYDFGDAQKTASYYSPIYGQREFTAGFVQFRVFNNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPOQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:**Signal peptide:**

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTCACCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT
CTGTCACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCCTTCTTCAT
ATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCCAGCTG
TCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAGAAACCCTTCTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACA
TTAAGACTTATATACAGTTTTAGGGGACAATTAAAAAAAAAAAA

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCCCTGGTGACGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCCTCCCGGCTCAGAGGACCCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCT
GGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCC
CACCCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAAGGTAGAACGGGGCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTAC
CATAGTGATACCCCTTACTACCCATCTGGGTGACCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGGAAGGGTTGGGCCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGTTCTTGCCATCCTGAGGAAAAGATAGCAACAGGGAGGGGGGAGATTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGTTCTCCCGGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGAGCATGTGCTGGATCTGTTC
TGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHS DTPYYPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAA
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGGGCTTTGGAATCATGA
GTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTC
TCCTGACCCACCTGCTGGTGTGTCAGCCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGAT
AACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIDNKG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLPGTVGIHGDSPOFFLYSAFMLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFILAAGGSCRSCLKCLLCQDKNFLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAACA
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTAC
CAATTTTTGTGCACACAACCTGGAGCCCAGGGCAGTATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCAGGAGCCTCATCATCCATTCCCTTGTTCCCGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
GAACCCCAGCAGGCCGCCCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTTTCAAATTTTTTCAACTAAGCTGCCTCGAATTTGGTGATACATGTGAATCTTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATTCTTAATT
TACCTGAAAATATTCTTGAAATTTCAGAAAATATGTTCTATGTAGAGAATCCCACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAACATATTTGGAAAACCTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLLIHSLEFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDEAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTGACCATG
GTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCCAGGCTCTCCCCAAGGCCCAGCCTGC
AGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACCTGACCAAGTTGC
CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTCAGGGGACTCAGGCAAGGCAACTGAG
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTTGCTGGTGACCAGGGCCCTGGACCGAGAGGA
GCAGGCAGAGTACCAGCTACAGGTCAACCTGGAGATGCAGGATGGACATGTCTTGTTGGGGTCCAC
AGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTGCCCATTTCTCTCAAGCCATCTAC
AGAGCTCGGCTGAGCCGGGTACCAGGCCTGGCATCCCCTTCTCTTCCCTTGAGGCTTCAGACCG
GGATGAGCCAGGCACAGCCAACCTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC
CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
CCAGGCCTCAGGCCACCAGGCCACTGCCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGT
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTTATACCCGCACCACATGGCCCAGGTA
CACTGGAGTGGGGGTGATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCTTTGAAGTGAA
TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCCAGGCTGAGTACCTGCTCC
AGGTGCGGGCTCAGAATTTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTG
ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
CAGTCCACCAGGTACTGAAGTGACTAGACTGTCAGCAGAGGATGCAGATGCCCCGGCTCCCCCA
ATTCCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
TCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGATTGGGCCT
ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCATTGATGCTGA
CCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTATGAG
GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCCC
AGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGAGTGATGCCACCCCCCAAGTTGG
ACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCCAGCCGGCTCTTTCCTGCTGACCATC
CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
CTGCATTGAGAAATTCTCCGGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
ACACCTACACGGTGCTTGTGGAGGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCCAA
TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCT
GGCCAGTGGGCACGGTCCCTACAGCTTACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGC
GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT
GAACACATAATCCCCGTGGTGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT
CGTGCTGCTGCAACGTGGAGGGGCAGTGCATGCGCAAGGTGGGCCGCATGAAGGGCATGCCCA
CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCCTGGTAGCAATAGGAATCTTCTCATCCTC
ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTT
GAAGGCGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAG
TCCCCTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCA
TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAACTT
TATGGAAGTGGCCATGGGAGTGTCCAAATGTGAGGTGTTTGGCCAAATAATAAAGCCCCAGAGAA
CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSVPQALPKAQPAELSVVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDQASGHQATATVEVSIIESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVLPPLRAGQNILLVLAMDLAGEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTEGTFGLDWEPPDSGHVRLRLCKNLSY
EAAPSHEVVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISRTRLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTLVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
TCTCTTCACTTTCAAGTCCCCTTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTAC
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCCAATGAGACTAGCACC
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
GCATAGTCACCAACTCTGAGTTCCATAACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCTCCAGTGGGGCCAGCACAGTCACCAACT
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCC
AGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCAC
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA
GCCACCAACTCTGACTCCAGCACAACTCCAGTGAGGCCAGCACAGCCACCAACTCTGAGTCTAG
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
ATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGGCAAAGCCTGGTGGGTCCCTGGT
GCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCTTAAGTGGTTCTGGAGGAGACCAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
ACAGCGGGCCCCTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCA
CCCAAGACCTGGTTTCTTTTTCATTTCATCCCAGGAGACCCCTCCAGCTTTGTTTGGATCCTGAA
AATCTTGAAGAAGGTATTCTCACCTTTCTTGCCCTTACCAGACACTGGAAAGAGAATACTATAT
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTG
CCCCGGGGTGGGTATCTAGCTCTGAGATGAAGTCACTTATAGGAGAAAACCTCCATGCTGGACTC
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES
STTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNSDSSTTSS
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA
TNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESSTVSSGISTVTNSES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRRPVSSI
AMEMSGRNNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTCACAGGTG
GGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTGTCATGGAAAGGGATTTACTTTTACTGACTCTGTTTTGGGGAAGCTTTTTTGGAAGCATTT
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCCACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAGT
GATTATAACTGGGGATGCATTTGTTCCCTGGAGAAAGAAGTGTCATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCCCTGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCCTCAAAGCGAGTCTCAAAGGTGTTCCCTGGATTTGGTTGGGCCATGCAGGCTGCTGCCTATAT
CTTCATTTCATAGGAAATGGAAGGATGACAAGAGCCATTTTGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAGGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACAACATTCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTCACGTCCACCGGTATCCAATAGACACCCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTC
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTTAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTTCATGACTATGTGAATATTTCTTACT
GCCATCATTATTTGTTAAAGATATTTTGCACCTTAATTTTGTGGGAAAAATATTGCTACAATTTTT
TTTAATCTCTGAATGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAAA

FIGURE 102

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFIMVSWKGIYFILTLFWGSFFGSIFMLSP
FLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
FLWNCLMRYSYLRLEKICLKASLKGVPFGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP
LQLLI FPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLLOGDFPREIH FHVHRYPIDTLPTSKE DLQLWCHKRWEEKERLRSFYQGEKNE
YFTGQSVIPPCKSELRLVLVVKLLSILYWTLESPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG
LEIIELACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTGCTCCCTCT
TTCTTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA
GTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTTCACTTCCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGGAAATCCAAGGTATTGATAGGAGAGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTA
TTTTACTCGGGTTACTCTGTGGTGCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGGAAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAAGTGTAAACCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGGATGACGTAGACAGGGGGAAGAACA
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT
ACATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCT
GGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGC
TGACATGTCAGTTTGAAGGCTTGTGAGACCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTCATATGTCCAGTGTCTGGGGATTGAGACAGAGAAGACCCTGCTTAAAGGGC
CCACACCCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCTGCTTACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTT
TGAGGGCACAGTGTGTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTT
TGCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC
CTCATTAACACAGACACAAAAATTCTAAATAAAATTTTAACAAATTAACTAAACAATATATTTA
AAGATGATATATACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAATATTTAAAT
ATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 104

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKT'VTHRKAQEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVLRLTTEHLYFT
FNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
TTTGTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA
CTCACTGTTTCATTATGTGAGATATAATCAAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC
TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGA
AACTGTAGATAAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
ATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGAGGGTGAATG
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
TTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
ATAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACA
TGACTATGATATTTCTCTTGACAGGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTC
TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT
GATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTTGCAATGAACC
TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGCAT
GCCAGGGTGACTCTGGAGGACCACTGGTTAGTTGAGATGCTAGAGATATCTGGTACCCTTGCTGGAATAGTG
AGCTGGGGAGATGAATGTGCGAAACCAACAAGCCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTG
GATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGT
GGTGTGGAGGCCATTTTATAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
ATAAACTGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
GATCAACTCTGTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
ATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTGTGAGAATTTGACTTGTGACATAAATTTGTAAT
GCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTCAGCTCCTCTCATTTACGCAAATATCCATTT
TCAAGGTGCAGAACAGGAGTGAAAGAAAAATATAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAA
AAGTATTAGGTGTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACA
GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG
ATATATCCTTATTTTCATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTGTGACCT
ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSVPYPYTNVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG
CCCCGATGAGCCCCCGCGTCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGGCCAGC
GCCGACGATCGCTGCCGTTTGGCCCTGGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
ACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCCGTGCCGTCTACGCCCTCAA
TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTIONACTTTCCCT
GTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGGATGTTAGGATATTG
TGAACGGGTGAAAAGAAATCTGTTGCTTCTTGCAATGGTACTTTGGAAGTTTGCTTGTCAATTTCT
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA
GATATGGTCACTTTGAAAGCCAGGATGACAAATTTATGGATTACCTAGATATCGGTGGCTTACTCA
TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGTCTGTGGAGTAGTATATTTCACTGACTGGTTGG
AAATGACAGAGATGGACTGGCCCCCAGATTCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAA
CAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTT
TTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGG
ACAGACCAAAATGATGTCCCTGAAGAATGACAACCTCTCAGCACCTGTCAATGTCCCTCAGTAGAACT
GTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
TTGAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACT
TGTGAATTTTTTGTAGTACATACTATGTGTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAA
TAACACCTAAGCATATACTATTCTATGCTTTAAAAATGAGGATGGAAAAGTTTCATGTCTAAGTC
ACCACCTGGACAATAATTGATGCCCTTAAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
TGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCA
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
CTCAGCGATCTATTCTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGGTGACT
ACCTAAATGTGATTTTTGCTGGTTACTAAAAATTTCTTACCCTTAAAAGAGCAAGCTAACACAT
TGTCTTAAGCTGATCAGGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT
TTCAGTTCTGATAATGTTAAGAAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATT
ATTTTTAGCCTTTCCCTGTTAATAAAGCTTTACTATTCTGTCCCTGGGCTTATATTACACATATAAC
TGTTATTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTC
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA
AAGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTGTACACTAAACACTTTTTAAAAA
GCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTTCTACAGAAAA
TAGTGTCTTTTTCTCCAGAAAAATGCTTGTGAGAAATCATTAAAACATGTGACAATTTAGAGATT
CTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATFACACAGATTATTAAATTTTTTTTACAA
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGTATTTTGTATTAT
TTCTCAGAATATGGAAAGAAAATTAATAATGTGTCAATAAATATTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCCCCTACCAGTGCT
GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCGCTCCATTCCCTGCTTCTCACCTG
CCTCTTCATCACAGGCACCTCCGTGTCACCCGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGC
CCTGGAGGAACACTGACCACCAGTTGGATGAGTCTCAAGTGCTCCTCTATGTGACAACCATGTGAATGGGGAG
TGGTACCACCTCACGGGCATGGCGGGAGATGCCATGCCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
TCAATGGGAAC TGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
CTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTTATGACATCTGCGACGAGGACTGCCATGG
CAGCTGCTCAGATAACCAGCGAGTGACATGCGCTCCAGGAAGTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGT
GAGTGTGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
TGGTGGCTGCAGCCACTCTTGCCCTTGGATCTGAGAAAGGCTACCAAGTGTGAATGTCCCGGGGCTGGTGCTGT
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
CTGGTTGGTGGCCTGGAGCTCTTCCTGACCAACACCTCCTGCCGAGGAGTGTCCAACGGCACCCATGTCAACAT
CCTCTTCTCTCTCAAGACATGTGGTACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
CAGGTCTACCCAAGCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG
ACCTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAAT
CATGAGCCGAAATCATGGGATCTTCCCATCACTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
GGGAAGCTCTGCCCCACCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGACGTGAGCGGC
TTGGAAGCTTGGTGGAGAGCTGCTTTGCCACCCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCAT
CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCAGCTTCCAGG
TCCCTGTCTTCAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTTCTGCACTGCCGGGTTCTTGTCTGTGGAGTG
TTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACGGCGGAATGCGTCGTGGGGCAGGAGGAGAGGACTCAGC
CGGTCTACAGGGCCAGACGCTAACAGGCGGCGCGATCCGCATCGACTGGGAGGACTAGTTCGTAGCCATACCTC
GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACC GCCCTCTAAGAACATCTGCCAACAGC
TGGGTTCAAGCTTCACACTGTGAGTTCAGACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCA
CAGGTCACAGCACTGCTGAACAATGTGGCCTGGGTGGGGTTTCATCTTCTAGGGTTGAAAATAAAGTGTCCA
CCAGAAAGACACTCACCCATTTCCCTCATTTCTTCTTACACTTAAATACCTCGTGTATGGTGCAATCAGAC
CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCTAGAAAAATTAAACAGTACTGAAATTATGA
CTTAAATACCCCAATGACTCCTTAAATATGTAATTTATAGTTATACCTTGAAATTTCAATTCAAATGCAGACTAA
TTATAGGGAATTTGGAAGTGTATCAATAAAACAGTATATAATTTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDQRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDVEGCHNNNGGCSHSCLGSEKGYQCECPRGLVLSEDNHTCQVPVLCKSNAIEVNI PRELVGG
LELFLTNTSCRGVSNGLTHVNILFSLKTCGTVVDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEPEPYREALPTLKLRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGP IRIDWED

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
CCTGCTGCCCTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCGTATCCCC
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTTGT
GGTTGTCCTCATCAAGGTGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
AGGGAAC TGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
GAGCTTCGCATGCGGAAC TCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCCTG
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGG
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCAGGGCA
GCCCCACTGCTTCAGGAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGSCAG
CTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAAGACAATGACA
TCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT
ACCAGGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGT
GACAGTGGTGGGCCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
CTGCGGGGGCCCCGAGCACCCCAAGGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
GGAAGGCTGAGCTGTAATGCTGCTGCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCT
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCCCACAGCCTCAGCAT
TTCTTGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCA
GCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
CAGGGGTATTGCTAAGCCAAGAAGGAAC TTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAA
GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
ACTGTTGTCTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAA
AAAA

FIGURE 112

MLQDPDS DQPLNSLDVKPLRKPRIPMETFRKVGIP I I I ALLSLAS I I IVVVL I KVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAE TACRQMGYSRAVEIGPDQDL DVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGGE EASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTA AHC FRKHTDVFNWKVRAGSDKL
GSFPSLAVAK I I I IEFNPMYPKDNDIALMKLQFP LTFSGTVRPICLPFFDEELTPATPLWIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCGDSGGPLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTTCAGCAACTAAAAAAGCCACAGGAGT
TGAAGTGTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAAAATC
TGTTTTTTGTTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAACTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGAGGCTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTTGACAAGCCCGAAGATTTCATAGGCGATGGCTCCCACTGCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCGGTGGACACCTGCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCGCCATCTAACCTTTTCATGTCTGCACATCACCTG
ATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTTATGTGACAGGACTTGCAATTCTCCTGGAACATGAGG
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTTGTGCCAAATTATGGGTTCAGAAAAGATG
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCAGTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTGGCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGTTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAAGAATTA
TGTTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
WPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATA
TTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGTGATTCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCCTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCTTGCCAACGAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTGTCGTGTCATCATGCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACA
TTATCACCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGGCGGGCGGCCAGGATCATGTCCACCACCACATGCCAAGTGGTGGCGTTCCCTCCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCT
GGGTGCCATTGGCCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGCAGACTGTTTCCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGGGGCTGGGTCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAGAAGAAACCAACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCAGCACTATGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCCAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCT
CGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCOCTC
TTCTCCTAGTCAATAAACCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTTGAAGGAAA
GAGTAGACCCAAAGATGTTATTTCTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGSAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTTGAGCTCTCCACFGGAGTCTCTTTCTGT
CGCGGGTCAGAAATGTCCCTAGATGAATGAGAAAATTATTTTAAATTTAAGTCCTAAATATAGTTAA
AATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAAACTAATTCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGGGAGTCC
AGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTTCTTG
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGGAGAGTGTCCGGCCTTCATT
GAAAAACAACATCGTGGTTTTTGAACCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
CATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTTTCTCCGGACCTACAGGCAGCCAGAG
GACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
ACCAGGTGCACGGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
CATCACGGGCATGGTGGTGCTCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATA
ACTCAATAGTGAATGTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCA
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTA
CAGATACTCGATACCTTCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG
TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCCAAATG
ACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGCCT
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAATGAGATA
TTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
CTCTTTTTTATCATTTTACTTCAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
ACGACATAGCATATGTACATAGATGAGTGTAAACATTTATATCTCACATAGAGACATGCTTATATGGT
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA
TTTATAATGAAGATTAATAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTT
CTTGTTGTTATTAATAACATTTTTTAAACGCAGATATTTTGTCAGGGGCTTTGCATTCAAACCTGCTT
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
AAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATA
TGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTA
CCATTTCTGTTTAGTTTTACTAAATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAA
ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTT
TATACATTTATATTAATAAATTTGTACATTTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQCK
IYDSLIALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG
CCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCC
GGGAGCCATGCGACCCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCCCAGGTCCGGATG
GATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTGGACACCCAACTAC
AAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGATACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAAGTGGCTCACTTCGGCTAAAATGCA
GAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATAAATGCTTTAATTTTCATTGCTACCTCTTTTTTTATTATGCC
TTGGAATGGTTCACTTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTG
CTTCAATCAAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTAA
AAAAATATAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPGR
DGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAI IYLDQGSPEMNSTINIHRTS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSR I I I EELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGGCTCCAACGCAGCTCTGTGGCTGAA
CTGGGTGCTCATCACGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
ATTGCCTGGAAGAAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTTTTTTTA
ACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAACGTAATATCCATGAAGATCC
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGAG
TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAGGGGTCCAATTTT
TCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTCTATGCAACTG
GCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG
CTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
ATCTCAGAAATTACAGGAGATACCCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
ATAACAGCCTTCAAAAACTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGA
GCTGATTCTTAGTTCGAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATT
TACGGAACCTGGATCTGTCTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA
AGACTGCCGCAACCTGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
TCTTTGCTGGCATGATCAGACTCAAAGAACCTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
CTGGCCCTTTTTTCCAAGGTTGGTCAGCCTTCAGAACCCTTACTTGCAAGTGAATAAAATCAGTGT
CATAGGACAGACCATGTCTTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGA
TCGAAGCTTTTCAAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT
TCCAACAAGCTCACATTTATTTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTT
TTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGGAGTAAATGTG
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGTTTGATCTGGCCAG
GGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCGAGCCGAAGCATGAGAGCAAACCCCTT
TGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTIAT
CTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCCAGCACCCAGGAATTTTATGTA
GATTATAAACCCACCAACACGGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCCCTGCACCTA
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAAGCT
GGGAAATAAGTGGTGCTTTATTGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCCTGTCCGTTTTAGTGCATTTCATAATACT
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
GAACTCCGGTTTAATATAATACCTATTGTATAAGACCCTTTACTGATTCCATTAAATGTCGATTT
GTTTTAAGATAAAACTTCTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPTIVLLTMLSSAERGCPKGCRCGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKELHLEHNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTMSWTWSSLQRLDL
SGNEIEAFSGPSVVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADAEHISFHKI IAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTTETSEMLLNGTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCCGAGCT
AGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAAGTGAAG
ATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
TTAGCCAATCCAAGTACCTAGTGAAGGTTTCAGATGCAAAATGGAAGGAAAAAGGAAACTGGAAGG
AAAACCATTGCGATTTTCGTGGTGTACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTGAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
ATCTTGGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES
APYRGMVRTALGIIEEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRRKLEGKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNQP
RDKQGRGLLYKSSTDCLIQAVQGEFGMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 127

CGCGGATCGGACCCAAGCAGGTGGCGGGCGGGCGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCGAC
CCCCGTGTGGGCTAGTCCAGCGAGGCGGACGGGCGGGCGTGGGCCCATGGCCAGGCCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCCCTCGGGGGGCATCGGCGCGGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCTACAGATGTGACCTAT
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCCACGGAGCAGGTGACCTAGTGACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTGCCTCTGGATTTTAGGTGTTGATTTCTGGAT
CACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGTTGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCTCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCAGTCTTGGCTTCTTGTTCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCAGTGGATTTTCATGGTGATCATTAAAAAGAAAAATCGCAACCAA
AAAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCA RTVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININSMGHRVPLSVTHFY SATKYAVTALTEGLRQELREAQTHIRATC
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AAC TTCTAC ATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTT CAGGTGCAGAGTCTCAGTTGCCCGGGAGC
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAAC TTGGGTGAATCACCGATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCA TTTCAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAAT GAGGGAAC TGAGAAAATTAATTTCTCATGTATTTTTCTCATTTATTTA
TTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACGGGGTTTTGCCATGTTGCCCAGG
CTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTTATGATTACA
GGCGTGAGCCACCGTGCCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGGAAC TTGAAATTAT
ACAATGAATTATTGTTAACTGT CATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTTGCTGCAAATGACAGGATTTCTGTTCTTAATTTCAATTAAAATAACCACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGGHTLGESPMFVKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
TCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATCGCTTTCCTGACATCCATTCCAACAG
GAATACCAGAGGATGCTACAACCTCTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTTCAGAT
TTGAAAACTTGCTGAAAGTAGAAAGAATATACCTATACCACAACAGTTTAGATGAATTTCTACCAACCT
CCCAAAGTATGTAAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
AAATTCCTATCTGGAAGAATTACATTTAGATGACAACCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCA
TTCCGAGACAGCAACTATCTCCGACTGCTTTTCCTGTCCCGTAATCACCTTAGCACAAATTCCTGGGGTTT
GCCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCATCTCTCAAG
GTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATTCCTGACTGCTGCACCAGTAAACCT
TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGCCCCAAATGCTTTTT
CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAA
AGGTTTCGTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAAGC
ACCATTCAAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAGCTCCAGTGAC
CAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAGGGAGTCCCTCAAGAAAAA
CAATTACAATTACTGTGAAGTCTGTCACCTCTGATACCATTCATATCTCTTGGAACCTTGCTCTACCTATG
ACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
AACAGGGGAACGCAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCCATATAAAGTATGCATGGTTC
CCATGGAAACCAGCAACCTCTACCTATTTGATGAACTCCTGTTTGATTGAGACTGAACTGCACCCCTT
CGAATGTACAACCCTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACC
TTTGGCTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGTATG
TTCATAGGAATGGATCGCTCTTCTCAAGGAACTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAACTTCTTTTCAGATGTTACCAAT
AAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAATACACACCATATTTCTCCTAATGGAATGAATCTGT
ACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCAGACTCAGATCAC
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATG
GT

FIGURE 132

MISAAWSIFLIGTKIGLFQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL
EELHLDNSVSAVSIEEGAFRDSNYLRLLFSLRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDL DNITQLILRNNPWYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD
IKNPKLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCIETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIALLLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKYNNHSESSNRSYRDSGIPDSDHSHS

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645**Amidation site.**

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGCCA
GCCCTGCCGGGGCCACTTGTCTTCAATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG
GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCGCTGTGGT
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
GCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
GGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCGGGAGAAGTGGGCCCAGGAGCCCCTGC
TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCAGCTGACCCCTCCAGCCCGG
GTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACAGTTCGGGC
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCCGGCTGCTC
AGGCTACTGCCTGTCCACCAACTGCTCTTCTCCTCTGGGCCAGAATGAGGGGATGCACACAGG
GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
AGAGCTGAGGGCCATCGGATACGCCTACCCTACCCGGGACATCTTCATGGAAAACATCATGTTCTG
TGGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
TATCAGCAGCATTTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGC
AATTCTCTTGCCATCCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAAT
TTTTATATTTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
CTCAAGAGATCCGCCCACCTCAGGCTCCCAAAGTGTTGGGATTATAGGTGTGAGCCACCGTGTCTG
GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
ATGGGGGCTCTCTCCCCTAGATGGCTGCTCCTCCCAACACAGCCACAGCAGTGGCAGCCCTGG
GTGGCTTCCTATACATCCTGGCAGAATACCCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
ATAAGCAAAGCCACCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

FIGURE 134

MSARGRWEGGRRACRGS LG LARAQGAERVTSSEQRPAMASLG LLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQ RSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSS EPCGLSDLCRSIMTKPGCSGYCLSHQLLFFLWARMRGCTQG PLQQSQD
YINLFCANMMDLNRRAEAIGYAYPTRDIEMENIMFCGMGGFSDFYKLRWLEAILS WQKQQEGCFG
EPDAEDEELSKAIQYQQHF SRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQF SCLILP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTTTCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTCGAGTGGATATCACCTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCATGAACCCAATGGT
TATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGGAACCGTGTGAAGCACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACCTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEAGSGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLKTDGSEFVVDIPSGSYVVEVVSPAYRFDVVRVDITSKGKMRARYVNYIKTSE
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLI FVLLPKVVNTSDPDMRREME
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSSKTGKSGAGKRR

Important features of the protein:**Signal sequence:**

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTCTCCCCAGTTCCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATCCCCAAAACAA
GTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA
AACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACATGCCATTGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAGGAGACAGAATTAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTG
CTTCCTTGCAATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTTCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTA
ATGTATTTATTTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTG
ACTAGAGCAGGTGATGTATTTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGG
CTAGGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAFTGTGTATCTTCCAG
CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAA
AAAAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPEIF
SSREAWQFFLLLWSPDFRPRMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTTCGGTTCCGCATCCAGCC
TAGCGTGTCCACGATGCGGCTGGGCTCCGGGACTTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
TAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCCCTCTGCCAGAGCGGAA
CACGGAGCGGAGCCCCAGCGCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG
GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAAAAAGGAGCATCTCACAGT
TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
CCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACCTGCTGGAAAGACAGTGTGA
TAAGACAAGCAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTTAAATTA
TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTTCGTGTCAGATTACACAGAGGT
GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC
TCCACTACCTGGGGCTGGACCACATTGGCCACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAG
AAGCTGAGCGAGATGGACAGCGTGCTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA
GACGCCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG
GGGCCTCCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAA
CCCGGTGATATCCGACATCCAAAGCACGTCCAATGACGGATGTGGCTGCGACACTGGCGATAGC
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGAC
CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAG
AATGTGCCGTCAATGAAAAAGATPCTTGGGTTTGAGCAGTTTAAATGTGAGAAAGATTGCATGG
GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTGAGAAGTCCTATTCAACCTGGGCTCCAAGG
TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCAG
TTCTCACCTGCTCCTGCTCAGCGTCCACAGGCACCTGCACAGAAAGGCTGAGCTGGAAGTCCCA
CTGTATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCGTTACGT
CATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTGGCGGCAGGCT
GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGGCAGTGCCCTGGAC
AGGGGGCCTCAGGGAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGGTGTCCCGACACAGGTG
TTCACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGGAAGCTAGGTTCTTGCAGCTGTTAC
CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
CACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACCACCTCATCCTGCCACCCCCAGAATGCATCCT
GCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGACGTTTTCTGTTGGAATTCTTAGTCCTTGGCC
TCGGACACCTTCATTGCTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
ACTCAGATCCACAGAGCCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
ACCCCAACCTGACAGCCCTCATCCCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGT
CTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTG
CCACGCTTGCACTCGGGCCCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAG
CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFEYDGTTSFFVSDYTEVDNNV
TRHLDKVLKRGDWDLILHYLGLDHHIGHISGPN SPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:**Signal peptide:**

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGT TACTGCTGCTGTTGGAGTACAAC
TCCCTATAGAAAACAAC TGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATT CATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCAATTTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAAC TAATTGTATAAAAACACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI
FFALASSLSSASAEKGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAAQKESARRPFI
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 33-36

N-myristoylation site.

amino acids 50-55, 87-92

Interleukin-1

amino acids 37-182

FIGURE 143

[illegible]

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGAACCGGAAGGCCCTGCCCAGCACTGCCCAGATCA
CTGAGGCCCAGGTGGCTGAGAACCGCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAAT
AAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCTGATAGATGGGGGACTGTGGCTTCT
CCGTCACCTCCATTCTCAGCCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCCTGCGCCACCTGCTTCACAGTACTTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTACAGATAAGGAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWLMVK

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATTT
CCTGATGATTTATAGACTCAAAGAAAACTATGTTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTTTGAAATTT
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGCTGAGG
TTTGGGGT

FIGURE 148

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 149

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCCGCCAGTCC
CGGCCCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTACTCCTCCTTTTCATTGATA
ACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACCTTGGATTCTGGTGTAGTGCTCCCGATTCAAGCTTTCCCCAAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAAAAGCCAGGTCAGAGCAACTATTCTTT
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTG
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCAACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGGAAGGAGAACTAAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTGAGAAAAAGAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAAACAAGCT
AGAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAAATGGCAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAAACATAATATAGCTTAAACACTTCTAATTCTGTGATTAAAAATTTTTGACCCAAGG
GTTATTAGAAAAGTGCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAAAACATAGCTTTCTTCCC
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 150

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLTTLTNGLE
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV
SYLENLDEMIALQTKNLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDK
EEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAAGGAACATTCTGAGGGGAGTCTACACCCTGTGGAGCTCAA
GATGGTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAG
CCAGTGCCTGTGCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCCCTGTGCACGGTGCCTGAAGCCGATCAGCC
TGTCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACTTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
GAGTGGAGGAGACCCATGGCGGACAATCACTCTCTCTGCTCTCAGGACCCCCACGTCTGACTTAG
TGGGCACCTGACCACCTTTGTCTTCTGGTTCACGTTTGGATAAATTCTGAGATTTGGAGCTCAGT
CCACGGTCTCTCCCCACTGGATGGTGCCTACTGCTGTGGAACCTTGTA AAAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTTCTGTGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCCCTGCT
TAATGGTAAC TGACAAGTGTTACCC TGAGCCCCG CAGGCCAACCCATCCCCAGTTGAGCCTTATA
GGGT CAGTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCC CAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCATA
TGCTACCTTTTCTATCTCTTCCCTCATCATCTTGTTGTGGGCATGAGGAGGTGGTGATGTCAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCCAA
GATACAATCAAAATCCCAGATGCTGGTCTCTAATCCCATGAAAAAGTGCTCATGACATATTGAGA
AGACCTACTTACAAAGTGGCATATATTGCAATTTAATTTAATTAAAAAGATAACCTATTTATATATT
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGTGGCAGTAT
AGGTGATTTTTCTTTTAAATCTGTTAATTTATCTGTATTTCCTAATTTTTCTACAATGAAGATGA
ATTCTTGATATAAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCCTCAGCCTCCACTTCCCAGAGTAAATTCAAATTGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAGGAAC TTAAAGAACAAAAATCATCTGGTAATCTTTTCTCTAGAA
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCATAT
GACTGGTTTCCCTTGATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGGAAGAGGCCAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCCGGCTGTTTTAA
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTAAAAATGATCCCTGT
CTCCTCGTGTTTACATTTCTGTGTGTGTCCCCCTCCCACAATGTACCAAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAATGAAGTCTCCT
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTTGGTCTAACTTGTTATGCAGCAATAGATAAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGGWNAIPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCCTGGCCACCAGCTGCCTCCTTCTCTTG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCAACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACTTCACCCCTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTT
CAGCCTTATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTTTAACCAAAAGGAAGATGGGAAGCCAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTATTGTAAGTGGTGTTT
TATACACAGAAAAACAATTTATTTTTTAAATAATTGTCTPTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFGVSMSERCYLMKQVLNFTLEEVLFPOSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCCGAGCATGTACCAGGTCAGTGCAGAGGGC
TGCCAGGCTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCCAGGACCTGTACCACGCCCCGT
TGCCCTGTGCCC GCACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGCGGCCCCGT
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCGTGGAAGTGCTGTCTGGAGCAG
CAGGATCCCGGGACAGGATGGGGGGCTTTGGGGAAACCTGCACCTTCTGCACATTTTGAAAAGAG
CAGCTGCTGCTTAGGGCCCGGGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAA
GTTCTGCCCATTTCTGGAGGCCACCACTCCTGTCTCTTCCCTCTTTCCCATCCCCTGCTACCCTG
GCCCAGCACAGGCACCTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATT
TGTTTGTTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTATTGAATGTATAGAGATTTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHTYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACACTAGTGTTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTTCATTGGGGCCCATATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTAAGAAGATGAGGAGACA
GTAGAAGTGAACCTTCACAACCACTCCCCTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGAAGTGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCAG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEHPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQQVSAGKRSQACHD
GCCSL

Important features of the protein:**Signal peptide:**

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCFTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

FIGURE 160

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVV
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

FIGURE 161

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGG
ACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATT
CAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGCAGCAC
AGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTTGCTGTCT
TGGCACTGGGGCCGAAGCCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACC
CACTGCTCTCCGGGCCTCTCCTGCCGCCCTCTGGGACAGTGACATACTCTGCCTGCCTGGGGACAT
CGTGCTGTCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCTGGTGCTGAGGTGCC
AGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGCCGTGCATGGGCACTGG
GAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGGGTGGAGGAGCCTAGGAA
TGCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCTACTGCCCGCTGCGTCTCTGC
TGGAGGTGCAAGTGCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATATGAC
TGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAA
GGAACCAACACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTCAGCAGATGGTGACA
ACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAG
GTCCAGGGCCCCCAAAACCCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAA
CCACACAGACCTGGTTCCCTGCCTCTGTATTTCAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGA
CGAACATCTGCCCTTCAGGGAGGACCCCCGCGCACACCAGAACCTCTGGCAAGCCGCCCGACTG
CGACTGCTGACCCTGCAGAGCTGGCTGCTGGACGCACCGTGTCTGCTGCCCGCAGAAGCGGCACT
GTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAACG
TCACTGTGGACAAGGTTCTCGAGTTCCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAGGTG
AACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGA
CGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAACCCA
GTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTA
CAAGACCTGCAGTCAGGCCAGTGCTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTG
CCCCATGGACAAATACATCCACAAGCGCTGGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCG
CTGCGCTTTCCCTCATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAA
CAGGACGTCCGCTCGGGGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGA
CTCGGGTTTCGAGCGCCTGGTGGGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGG
CCGTAGACCTGTGGAGCCGTCTGTGAAGTGAAGCGCGCAGGGGCCCGTGGCTTGGTTTCACGCGCAG
CGGCGCCAGACCTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCCGGTGCGGTGGCGCT
GTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGGCCGGGGCGCACGGCCCGCACGACGCCTTCC
GCGCCTCGCTCAGCTGCGTGCTGCCCCGACTTCTTGCAAGGGCCGGGCGCCCGGCAGCTACGTGGGG
GCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGCACCGTGCCCGTCTT
CACACTGCCCTCCCAACTGCCAGACTTCCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCGTTCGG
GGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGGCCCTTCAGCCAGCCCTGGATAGCTACTTC
CATCCCCCGGGGACTCCCGCGCGGGACGCGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGA
CGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

FIGURE 162

MPVPWFLLSLALGRSPVVLSELRLVGPQDATHCSPGLSCRLWDSDIICLPGDIVPAPGPVLAPTHLQTELV
LRCQKETDCDLCRLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSTFQAYPTARCVLLEV
QVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYTPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNV
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQQLQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLLLKQDVRSGAAARG
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT
LPSQLPDFLGALQQPRAPRSGRLLQERAEQVSRLQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA
AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCACAGACACGGTCTACAGCATCGAGTATA
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTGAGCGGATCACCCGGAAGTCCTGC
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
GTCAGTGCGGGAGGCCGGTCAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC
CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA
CCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCCCTGGAAGACATCTTCCATGACCTG
TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
ATATGAGTTCCTCGGCCTGACCCCTGACACAGAGTTCTTGGCACCATCATGATTTGCGTTCCCA
CCTGGGCCAAGGAGAGTGGCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
TACTCCTTCTCCGGAGCCTTCTGTCTCCATGGGCTTCTCGTCGCAGTACTCTGCTACCTGAG
CTACAGATATGTACCAAGCCGCCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCTTGACTT
TCCAGCCGCTGCGCTTCATCCAGGAGCACGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC
AGTCTGGCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCCGAGGAGC
TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCCACTGTCTATGCCCAAACGCTGCCCTGAG
GTCGGGCCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTTACGCCCCACA
GGCCATCTCTAAGGTCCAGCCTTCTCCTATGCCCTCAAGCCACTCCGGACAGCTGGCCTCCCT
CCTATGGGGTATGCATGGAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTTAAA
CACCCTTAGGCCTAAAGGTCAGCTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCCT
TTCTCTGCAGGAGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGACCCAGC
CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCCATGTC
CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCCGAGACCTCAGACCTG
GAGCAGCCCACAGAACTGGATTCTCTTTTCAGAGGCCTGGCCCTGACTGTGCAGTGGGAGTCCTG
AGGGGAATGGGAAAGGCTTGGTGCTTCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
ATCCCATGCCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
AGGACTGCAGCGGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGGTGCTCGCTGAGCCCTG
CAAGGCAGAAATGACAGTGCAAGGAGGAAATGCAGGGAAACTCCCGAGGTCCAGAGCCCCACCTC
CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGCCCCATTCTTGCCAGTTTC
ACAATCTAGCTCGACAGAGCATGAGGCCCTGCCTCTTCTGTGATTGTTCAAAGGTGGGAAGAGA
GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAAGCAACCTGC
ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
TTCCCAGCCAGGGCAACTGCCTGACGTTGCACGATTTGAGCTTCATTCTCTGATAGAACAAAGC
GAAATGCAGSTCCACCAGGGAGGGAGACACACAAGCCTTTTCTGCAGGCAGGAGTTTCAGACCCCT
ATCCTGAGAATGGGGTTTGAAAGGAAGGTGAGGGCTGTGGCCCCCTGGACGGGTACAATAACACAC
TGTAAGTATGTACAACCTTTGCAAGCTCTGCCTTGGGTTGAGCCCATCTGGGCTCAAATTTCCAGC
CTCACCCTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCTCTC
ATCTGTAATGTGGGATCATAACACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
TCTTTAAAGTGCTTAATAGTGCTGGTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAAA
AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTLEYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVTCIS
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
PNSLVQRVLTFQPLRFIQEHVLIPVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAISKVQPSSY
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLQKEPPAGSCMLGGLSLQEVTSLAM
EESQEAKSLHQPLGICTDRTSDPNVLHSGEETPGQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC
SPSDQGPSPWGLLESLVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTVQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGCTGGGGGCGCTCTGGTGGSTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACTTTGGGCTGGA
AGTGTGTAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCCCTGTGCCTGAGCCCGAGGCATTTCAGAGCTGATTTCAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATCTGCACGATAA
ATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT
CATTACAGCAAAGGATTTCTGTTGGCATCAAAATCTAAGTTTGTTTTACAAAGATTGTTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCCAAACAAAATATATTTATTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFVLGALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPDCRFVN
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETDFVCFEGGRD
DFNSYNVEELLGSLELED SVPEESKKAEEVSQHREKSP EESRGRELDPVPEPEAFRA DSEDEGEA
FSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVP GSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCTAACTTC
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCGCGTGGTCAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT
GTCCAGCCGAGTGAGCTTTTCAAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCTCTCTCA
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG
TGCCTGCCCAGATCTCTACCAAGTGGTCTGATGGAAGCAATTCACAGTACCGAAACTGGTACACAG
ATGAACCTTCTCGCGAAGTGAAAAGTGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACCAAGTGGAAATGATGACAGGTGTAACATGAAGCACAATTATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG
GAGACACCCATCAGAAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
ATACCAACAATAACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCT
GCATAAAAAGTAAAGGAAGAACAATACTAGTCCAAACAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAATTCT
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGC
AAGATGAAGTGAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTATATGTCTATTATTTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTTACCTTTTCATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAA
ATGAAGTGTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
AATAAGAAGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATGTGCAAGACATGTGCCTTATAATTATTTTAGCTTAAAATTAAACAGATT
TTGTAATAATGTAACCTTGTAAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCTATATAATGAGAAGCAGCTCTCTGA
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAAATGGGTGG
AACCCTATCAGTGATCGCATATTCATTGATGAGGGTTTGTCTTGAGATAGAAAATGGTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTCAAGAGAAAGTTGTAAGTCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFRRVVSQGKVCFADEKHPCKMAYFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDWIGLWRNGDGGTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKTSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-
145, 212-217

1

SECRETED POLYPEPTIDE OVEREXPRESSED IN RECTAL TUMOR

RELATED APPLICATIONS

This application is a continuation of, and claims priority under 35 USC §120 to, U.S. application Ser. No. 10/006,867 filed Dec. 6, 2001, which is a continuation of, and claims priority under 35 USC §120 to, PCT Application PCT/US00/23328 filed Aug. 24, 2000.

BACKGROUND OF THE INVENTION

The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Pat. No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and nerve growth factor receptor.

2

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF INVENTION

In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

3

least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least

4

about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the peptide, as

disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment

of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes useful for isolating genomic and cDNA nucleotide sequences or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF DRAWINGS

FIG. 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO180 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA26843-1389".

FIG. 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in FIG. 1.

FIG. 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO218 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA30867-1335".

FIG. 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in FIG. 3.

FIG. 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO263 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA34431-1177".

FIG. 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in FIG. 5.

FIG. 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO295 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA38268-1188".

FIG. 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in FIG. 7.

FIG. 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO874 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA40621-1440".

FIG. 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in FIG. 9.

FIG. 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO300 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA40625-1189".

FIG. 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in FIG. 11.

FIG. 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO1864 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA45409-2511".

FIG. 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in FIG. 13.

FIG. 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO1282 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA45495-1550".

FIG. 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in FIG. 15.

FIG. 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO1063 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA49820-1427".

FIG. 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in FIG. 17.

FIG. 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO1773 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA56406-1704".

FIG. 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in FIG. 19.

FIG. 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO1013 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA56410-1414".

FIG. 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in FIG. 21.

FIG. 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO937 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA56436-1448".

FIG. 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in FIG. 23.

FIG. 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO842 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA56855-1447".

FIG. 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in FIG. 25.

FIG. 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO1180 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA56860-1510".

FIG. 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in FIG. 27.

FIG. 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO831 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA56862-1343".

FIG. 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in FIG. 29.

FIG. 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO1115 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA56868-1478".

FIG. 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in FIG. 31.

FIG. 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO1277 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA56869-1545".

FIG. 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in FIG. 33.

FIG. 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO1074 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA57704-1452".

FIG. 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in FIG. 35.

FIG. 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO1344 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA58723-1588".

FIG. 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in FIG. 37.

FIG. 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO1136 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA57827-1493".

FIG. 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in FIG. 39.

FIG. 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO1109 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA58737-1473".

FIG. 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in FIG. 41.

FIG. 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO1003 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA58846-1409".

FIG. 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in FIG. 43.

FIG. 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO1138 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA58850-1495".

FIG. 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in FIG. 45.

FIG. 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO994 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA58855-1422".

FIG. 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in FIG. 47.

FIG. 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO1069 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA59211-1450".

FIG. 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in FIG. 49.

FIG. 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA59212-1627".

FIG. 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in FIG. 51.

FIG. 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO1129 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA59213-1487".

FIG. 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in FIG. 53.

FIG. 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO1027 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA59605-1418".

FIG. 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in FIG. 55.

FIG. 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO1106 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA59609-1470".

FIG. 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in FIG. 57.

FIG. 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO1291 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA59610-1556".

FIG. 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in FIG. 59.

FIG. 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO3573 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA59837-2545".

FIG. 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in FIG. 61.

FIG. 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO3566 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA59844-2542".

FIG. 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in FIG. 63.

FIG. 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1098 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA59854-1459".

FIG. 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in FIG. 65.

FIG. 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO1158 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA60625-1507".

FIG. 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in FIG. 67.

FIG. 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO1124 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA60629-1481".

FIG. 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in FIG. 69.

FIG. 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO1287 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA61755-1554".

FIG. 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in FIG. 71.

FIG. 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO1335 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA62812-1594".

FIG. 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in FIG. 73.

FIG. 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO1315 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA62815-1576".

FIG. 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in FIG. 75.

FIG. 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO1357 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA64881-1602".

FIG. 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in FIG. 77.

FIG. 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO1356 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA64886-1601".

FIG. 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in FIG. 79.

FIG. 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO1557 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA64902-1667".

FIG. 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in FIG. 81.

FIG. 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO1347 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA64950-1590".

FIG. 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in FIG. 83.

FIG. 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO1302 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA65403-1565".

FIG. 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in FIG. 85.

FIG. 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO1270 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA66308-1537".

FIG. 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in FIG. 87.

FIG. 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO1268 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA66519-1535".

FIG. 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in FIG. 89.

FIG. 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO1327 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA66521-1583".

FIG. 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in FIG. 91.

FIG. 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO1328 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA66658-1584".

FIG. 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in FIG. 93.

FIG. 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA66660-1585".

FIG. 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in FIG. 95.

FIG. 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO1340 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA66663-1598".

FIG. 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in FIG. 97.

11

FIG. 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO1342 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA66674-1599".

FIG. 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in FIG. 99.

FIG. 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO3579 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA68862-2546".

FIG. 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in FIG. 101.

FIG. 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO1472 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA68866-1644".

FIG. 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in FIG. 103.

FIG. 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO1461 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA68871-1638".

FIG. 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in FIG. 105.

FIG. 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1568 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA68880-1676".

FIG. 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in FIG. 107.

FIG. 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1753 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA68883-1691".

FIG. 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in FIG. 109.

FIG. 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO1570 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA68885-1678".

FIG. 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in FIG. 111.

FIG. 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO1446 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA71277-1636".

FIG. 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in FIG. 113.

FIG. 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO1565 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA73727-1673".

FIG. 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in FIG. 115.

FIG. 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO1572 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA73734-1680".

FIG. 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in FIG. 117.

FIG. 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA73735-1681".

FIG. 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in FIG. 119.

12

FIG. 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO1550 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA76393-1664".

FIG. 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in FIG. 121.

FIG. 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO1693 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA77301-1708".

FIG. 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in FIG. 123.

FIG. 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO1566 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA77568-1626".

FIG. 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in FIG. 125.

FIG. 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO1774 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA77626-1705".

FIG. 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in FIG. 127.

FIG. 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA81754-2532".

FIG. 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in FIG. 129.

FIG. 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1865 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA81757-2512".

FIG. 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in FIG. 131.

FIG. 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1925 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA82302-2529".

FIG. 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in FIG. 133.

FIG. 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO1926 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA82340-2530".

FIG. 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in FIG. 135.

FIG. 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA83500-2506".

FIG. 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in FIG. 137.

FIG. 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO4405 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA84920-2614".

FIG. 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in FIG. 139.

FIG. 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO3435 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA85066-2534".

FIG. 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in FIG. 141.

13

FIG. 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO3543 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA86571-2551".

FIG. 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in FIG. 143.

FIG. 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO3443 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA87991-2540".

FIG. 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in FIG. 145.

FIG. 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO3442 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA92238-2539".

FIG. 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in FIG. 147.

FIG. 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO5990 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA96042-2682".

FIG. 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in FIG. 149.

FIG. 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO4342 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA96787-2534".

FIG. 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in FIG. 151.

FIG. 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO10096 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA125185-2806".

FIG. 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in FIG. 153.

FIG. 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO10272 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA147531-2821".

FIG. 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in FIG. 155.

FIG. 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO5801 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA115291-2681".

FIG. 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in FIG. 157.

FIG. 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO20110 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA166819".

FIG. 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in FIG. 159.

FIG. 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO20040 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA164625-2890".

FIG. 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in FIG. 161.

FIG. 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO20233 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA165608".

14

FIG. 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in FIG. 163.

FIG. 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO19670 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA131639-2874".

FIG. 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in FIG. 165.

FIG. 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1890 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA79230-2525".

FIG. 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in FIG. 167.

DETAILED DESCRIPTION

I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

15

The PRO polypeptide “extracellular domain” or “ECD” refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the “signal peptides” of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., *Prot. Eng.* 10:1–6 (1997) and von Heinje et al., *Nucl. Acids. Res.* 14:4683–4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

“PRO polypeptide variant” means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino

16

acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

“Percent (%) amino acid sequence identity” with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from

the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from the National Institutes of Health website or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from the National Institutes of Health website or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid

sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the

source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the

comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide in situ within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid

molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions

more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., *Current Protocols in Molecular Biology*, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50° C.; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42° C.; or (3) employ 50% formamide, 5×SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5× Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42° C., with washes at 42° C. in 0.2×SSC (sodium chloride/sodium citrate) and 50% formamide at 55° C., followed by a high-stringency wash consisting of 0.1×SSC containing EDTA at 55° C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and % SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37° C. in a solution comprising: 20% formamide, 5×SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5× Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1×SSC at about 37–50° C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain

sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are non-toxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic

polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, polyethylene glycol (PEG), and PLURONICTM.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062[1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol.113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Pat. No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      .8      /* value of a match with a stop */

int      _day[26][26] = {
/*      A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */      { 2, 0, 0, 0, 0, 4, 1, 1, 1, 0, 1, 2, 1, 0, _M, 1, 0, 2, 1, 1, 0, 0, 6, 0, 3, 0},
/* B */      { 0, 3, 4, 3, 2, 5, 0, 1, 2, 0, 0, 3, 2, 2, _M, 1, 1, 0, 0, 0, 0, 2, 5, 0, 3, 1},
/* C */      { 2, 4, 15, 5, 5, 4, 3, 3, 2, 0, 5, 6, 5, 4, _M, 3, 5, 4, 0, 2, 0, 2, 8, 0, 0, 5},
/* D */      { 0, 3, 5, 4, 3, 6, 1, 1, 2, 0, 0, 4, 3, 2, _M, 1, 2, 1, 0, 0, 0, 2, 7, 0, 4, 2},
/* E */      { 0, 2, 5, 3, 4, 5, 0, 1, 2, 0, 0, 3, 2, 1, _M, 1, 2, 1, 0, 0, 0, 2, 7, 0, 4, 3},
/* F */      { 4, 5, 4, 6, 5, 9, 5, 2, 1, 0, 5, 2, 0, 4, _M, 5, 5, 4, 3, 3, 0, 1, 0, 0, 7, 5},
/* G */      { 1, 0, 3, 1, 0, 5, 5, 2, 3, 0, 2, 4, 3, 0, _M, 1, 1, 3, 1, 0, 0, 1, 7, 0, 5, 0},
/* H */      { 1, 1, 3, 1, 1, 2, 2, 6, 2, 0, 0, 2, 2, 2, _M, 0, 3, 2, 1, 1, 0, 2, 3, 0, 0, 2},
/* I */      { 1, 2, 2, 2, 2, 1, 3, 2, 5, 0, 2, 2, 2, 2, _M, 2, 2, 2, 1, 0, 0, 4, 5, 0, 1, 2},
/* J */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */      { 1, 0, 5, 0, 0, 5, 2, 0, 2, 0, 5, 3, 0, 1, _M, 1, 1, 3, 0, 0, 0, 2, 3, 0, 4, 0},
/* L */      { 2, 3, 6, 4, 3, 2, 4, 2, 2, 0, 3, 6, 4, 3, _M, 3, 2, 3, 3, 1, 0, 2, 2, 0, 1, 2},
/* M */      { 1, 2, 5, 3, 2, 0, 3, 2, 2, 0, 0, 4, 6, 2, _M, 2, 1, 0, 2, 1, 0, 2, 4, 0, 2, 1},
/* N */      { 0, 2, 4, 2, 1, 4, 0, 2, 2, 0, 1, 3, 2, 2, _M, 1, 1, 0, 1, 0, 0, 2, 4, 0, 2, 1},
/* O */      { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */      { 1, 1, 3, 1, 1, 5, 1, 0, 2, 0, 1, 3, 2, 1, _M, 6, 0, 0, 1, 0, 0, 1, 6, 0, 5, 0},
/* Q */      { 0, 1, 5, 2, 2, 5, 1, 3, 2, 0, 1, 2, 1, 1, _M, 0, 4, 1, 1, 1, 0, 2, 5, 0, 4, 3},
/* R */      { 2, 0, 4, 1, 1, 4, 3, 2, 2, 0, 3, 3, 0, 0, _M, 0, 1, 6, 0, 1, 0, 2, 2, 0, 4, 0},
/* S */      { 1, 0, 0, 0, 0, 3, 1, 1, 1, 0, 0, 3, 2, 1, _M, 1, 1, 0, 2, 1, 0, 1, 2, 0, 3, 0},
/* T */      { 1, 0, 2, 0, 0, 3, 0, 1, 0, 0, 0, 1, 1, 0, _M, 0, 1, 1, 1, 3, 0, 0, 5, 0, 3, 0},
/* U */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */      { 0, 2, 2, 2, 2, 1, 1, 2, 4, 0, 2, 2, 2, 2, _M, 1, 2, 2, 1, 0, 0, 4, 6, 0, 2, 2},
/* W */      { 6, 5, 8, 7, 7, 0, 7, 3, 5, 0, 3, 2, 4, 4, _M, 6, 5, 2, 2, 5, 0, 6, 17, 0, 0, 6},
/* X */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */      { 3, 3, 0, 4, 4, 7, 5, 0, 1, 0, 4, 1, 2, 2, _M, 5, 4, 4, 3, 3, 0, 2, 0, 0, 10, 4},
/* Z */      { 0, 1, 5, 2, 3, 5, 0, 2, 2, 0, 0, 2, 1, 1, _M, 0, 3, 0, 0, 0, 0, 2, 6, 0, 4, 4}
}

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

#define MAXJMP 16      /* max jumps in a diag */
#define MAXGAP 24      /* don't continue to penalize gaps larger than this */
#define JMPS 1024      /* max jmps in an path */
#define MX 4          /* save if there's at least MX-1 bases since last jmp */

#define DMAT 3         /* value of matching bases */
#define DMIS 0         /* penalty for mismatched bases */
#define DINSO 8        /* penalty for a gap */
#define DINS1 1        /* penalty per base */
#define PINSO 8        /* penalty for a gap */
#define PINS1 4        /* penalty per residue */

struct jmp {
    short          n[MAXJMP];      /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP];      /* base no. of jmp in seq x */
};

struct diag {
    int            score;          /* score at last jmp */
    long           offset;         /* offset of prev block */
    short          ijmp;          /* current jmp index */
    struct jmp     jp;            /* list of jmps */
};

struct path {
    int            spc;            /* number of leading spaces */
    short          n[JMP];        /* size of jmp (gap) */
    int            x[JMP];        /* loc of jmp (last elem before gap) */
};

char             *ofile;          /* output file name */
char             *namex[2];       /* seq names: getseqs() */
char             *prog;           /* prog name for err msgs */
char             *seqx[2];        /* seqs: getseqs() */
int              dmax;            /* best diag: nw() */
int              dmax0;           /* final diag */
int              dna;             /* set if dna: main() */
int              endgaps;         /* set if penalizing end gaps */
int              gapx, gapy;       /* total gaps in seqs */
int              len0, len1;       /* seq lens */
int              ngapx, ngapy;     /* total size of gaps */
int              smax;            /* maxscore: nw() */
int              *xbm;            /* bitmap for matching */
long             offset;          /* current offset in jmp file */
struct diag      *dx;             /* holds diagonals */
struct path      pp[2];           /* holds path for seqs */

char             *calloc(), *malloc(), *index(), *strcpy();
char             *getseq(), *g_calloc();

```


Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: prog file1 file2
* where file1 and file2 are two dna or two protein sequences.
* The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with '!', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
* Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
#include "day.h"

static  _dbval[26] = {
1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static  _pbval[26] = {
1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
int      ac;
char     *av[];
{
    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lowercase\n");
        fprintf(stderr, "Any lines beginning with '!' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file 'align.out'\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0; /* 1 to penalize endgaps */
    ofile = "align.out"; /* output file */

    nw(); /* fill in the matrix, get the possible jmps */
    readjmps(); /* get the actual jmps */
    print(); /* print stats, alignment */

    cleanup(); /* unlink any tmp files */
}

```

main

Table 1 (cont')

```

/* do the alignment, return best score main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */

nw()
{
    char      *px, *py;          /* seqs and ptrs */
    int        *ndely, *dely;     /* keep track of dely */
    int        ndelx, delx;       /* keep track of delx */
    int        *tmp;              /* for swapping row0, row1 */
    int        mis;               /* score for each type */
    int        ins0, ins1;        /* insertion penalties */
    register   id;                /* diagonal index */
    register   ij;                /* jmp index */
    register   *col0, *col1;      /* score for curr, last row */
    register   xx, yy;            /* index into seqs */

    dx = (struct diag *)g_calloc("to get diag", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
     */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
         */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```

nw

Table 1 (cont')

...NW

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px'A'] & xbm[*py'A'])? DMAT : DMIS;
    else
        mis += _day[*px'A'][*py'A'];

    /* update penalty for del in x seq;
     * favor new del over ongoing del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongoing del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */

```

Table 1 (cont')

...dw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
else if (delx >= dely[yy]) {
    coll[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejmps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
    }
    else {
        coll[yy] = dely[yy];
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejmps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
                offset += sizeof(struct jmp) + sizeof(offset);
            }
            dx[id].jp.n[ij] = ndely[yy];
            dx[id].jp.x[ij] = xx;
            dx[id].score = dely[yy];
        }
        if (xx == len0 && yy < len1) {
            /* last col
            */
            if (endgaps)
                coll[yy] -= ins0+ins1*(len1-yy);
            if (coll[yy] > smax) {
                smax = coll[yy];
                dmax = id;
            }
        }
    }
}
if (endgaps && xx < len0)
    coll[yy-1] -= ins0+ins1*(len0-xx);
if (coll[yy-1] > smax) {
    smax = coll[yy-1];
    dmax = id;
}
}
tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);

```

```
(void) free((char *)col0);  
(void) free((char *)col1);
```

}

Table 1 (cont')

```

/*
 *
 * print() ~ only routine visible outside this module
 *
 * static:
 * getmat() ~ trace back best path, count matches: print()
 * pr_align() ~ print alignment of described in array p[]: print()
 * dumpblock() ~ dump a block of lines with numbers, stars: pr_align()
 * nums() ~ put out a number line: dumpblock()
 * putline() ~ put out a line (name, [num], seq, [num]): dumpblock()
 * stars() ~ put a line of stars: dumpblock()
 * stripname() ~ strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC      3
#define P_LINE  256    /* maximum output line */
#define P_SPC    3      /* space between name or num and seq */

extern  _day[26][26];
int     olen;          /* set output line length */
FILE    *fx;           /* output file */

print()
{
    int     lx, ly, firstgap, lastgap;    /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) {          /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) {     /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) {        /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) {   /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

print

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
    int      lx, ly;          /* "core" (minus endgaps) */
    int      firstgap, lastgap; /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
    char      out[32];
    double    pct;
    register  n0, n1;
    register char *p0, *p1;

    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while (*p0 && *p1) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A'] & xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100. * (double)nm / (double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%es in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);

```

getmat

Table 1 (cont')

```

fprintf(fx, "<gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapx, (dna)? "base": "residue", (ngapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
            ngapy, (dna)? "base": "residue", (ngapy == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINSO, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINSO, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base": "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base": "residue", (lastgap == 1)? "" : "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}

static      nm;          /* matches in core - for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number ~ for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output charslot */
static char out[2][P_LINE]; /* output line */
static char stat[P_LINE]; /* set by stats */

/*
 * print alignment of described in struct path pp []
 */
static
pr_align0
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(nameex[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
    }
}

```

...getmat

pr_align

47

```
ps[i] = seqx[i];  
po[i] = out[i];
```

48

}

Table 1 (cont.)

```

for (nn = nm = 0, more = 1; more;) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;

        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = ' ';
            siz[i]--;
        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;

            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i]++];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]++];
            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;

```

...pr_align

dumpblock

```
for (i = 0; i < 2; i++)  
    *p0[i] = '\0';
```

Table 1 (cont')

...dumpblock

```

(void) putc('\n', fx);
for (i = 0; i < 2; i++) {
    if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
        if (i == 0)
            nums(i);
        if (i == 0 && *out[i])
            stars();
        putline(i);
        if (i == 0 && *out[i])
            fprintf(fx, star);
        if (i == 1)
            nums(i);
    }
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
    int ix; /* index in out[] holding seq line */
{
    char nline[P_LINE];
    register i, j;
    register char *pn, *px, *py;

    for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '\t')
            *pn = ' ';
        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j; j /= 10, px--)
                    *px = j%10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = *py;
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static

```

nums

55

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putline(ix)
int

ix;

{

putline

Table 1 (cont')

...putline

```

int          i;
register char *px;

for (px = names[ix], i = 0; *px && *px != '\0'; px++, i++)
    (void) putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void) putc(' ', fx);

/* these count from 1:
 * ni[] is current element (from 1)
 * nc[] is number at start of current line
 */
for (px = out[ix]; *px; px++)
    (void) putc(*px&0x7F, fx);
(void) putc('\n', fx);
}

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
{
    int          i;
    register char *p0, *p1, cx, *px;

    if (!(*out[0] || (*out[0] == '\0' && (*p0[0] == '\0') ||
        !*out[1] || (*out[1] == '\0' && (*p1[1] == '\0'))
        return;
    px = star;
    for (i = lmax+P_SPC; i; i--)
        *px++ = ' ';

    for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
        if (isalpha(*p0) && isalpha(*p1)) {
            if (xbrn[*p0-'A'] && xbrn[*p1-'A']) {
                cx = '"';
                nm++;
            }
            else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                cx = '!';
            else
                cx = ' ';
        }
        else
            cx = ' ';
        *px++ = cx;
    }
    *px++ = '\n';
    *px = '\0';
}

```

stars

Table 1 (cont')

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
    char    *pn;    /* file name (maybe path) */
{
    register char    *px, *py;

    py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
    if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}

```

stripname

Table 1 (cont')

```

/*
 * cleanup() - cleanup any tmp file
 * getseq() - read in seq, set dna, len, maxlen
 * g_alloc() - calloc() with error checkin
 * readjimps() - get the good jimps, from tmp file if necessary
 * writejimps() - write a filled array of jimps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jimps */
FILE     *fj;

int      cleanup();                          /* cleanup tmp file */
long     lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)
    int    i;
{
    if (fj)
        (void) unlink(jname);
    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with '|', '<', or '>'
 * seq in upper or lower case
 */
char      *
getseq(file, len)
    char    *file;      /* file name */
    int     *len;        /* seq len */
{
    char      line[1024], *pseq;
    register char *px, *py;
    int       natgc, tlen;
    FILE      *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == '|' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

cleanup

getseq

Table 1 (cont')

```

py = pseq + 4;
*len = tlen;
rewind(fp);

while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU",*(py-1)))
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return (pseq+4);
}

char *
g_calloc(msg, nx, sz)
char *msg;          /* program, calling routine */
int nx, sz;          /* number and size of elements */
{
    char *px, *calloc0;

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return (px);
}

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
{
    int fd = -1;
    int siz, f0, i1;
    register i, j, xx;

    if (f) {
        (void) fclose(f);
        if (((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
        while (1) {

```

...getseq

g_calloc

readjmps

```
for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].ip.x[j] >= xx; j-)  
    ;
```

Table 1 (cont')

...readjumps

```

    if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
    }
    else
        break;
}
if (i >= JMPS) {
    fprintf(stderr, "%s: too many gaps in alignment\n", prog);
    cleanup(1);
}
if (j >= 0) {
    siz = dx[dmax].jp.n[j];
    xx = dx[dmax].jp.x[j];
    dmax += siz;
    if (siz < 0) { /* gap in second seq */
        pp[1].n[i1] = -siz;
        xx += siz;
        /* id = xx - yy + len1 - 1 */
        /*
        pp[1].x[i1] = xx - dmax + len1 - 1;
        gapy++;
        ngapy -= siz;
        */
        /* ignore MAXGAP when doing endgaps */
        siz = (siz < MAXGAP || endgaps) ? siz : MAXGAP;
        i1++;
    }
    else if (siz > 0) { /* gap in first seq */
        pp[0].n[i0] = siz;
        pp[0].x[i0] = xx;
        gapx++;
        ngapx += siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (siz < MAXGAP || endgaps) ? siz : MAXGAP;
        i0++;
    }
}
else
    break;
}

/* reverse the order of jumps */
/*
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
}

```

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offset = 0;

}

}

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejumps(ix)
{
    int ix;
    char *mktemp0;

    if (!fj) {
        if (mktemp(jname) < 0) {
            fprintf(stderr, "%s: can't mktemp0 %s\n", prog, jname);
            cleanup(1);
        }
        if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
    }
    (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
    (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}

```

writejumps

TABLE 2

PRO	XXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 15 = 33.3%

TABLE 3

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXXXYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 10 = 50%

TABLE 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 6 divided by 14 = 42.9%

TABLE 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Pat. No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

TABLE 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- (1) hydrophobic: norleucine, met, ala, val, leu, ile;
- (2) neutral hydrophilic: cys, ser, thr;
- (3) acidic: asp, glu;
- (4) basic: asn, gln, his, lys, arg;
- (5) residues that influence chain orientation: gly, pro; and
- (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al., Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins,

(W. H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis (diazooacetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis (succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propionimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T. E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 Sep. 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal.

Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also U.S. Pat. No. 5,428,130 issued Jun. 27, 1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., *Solid-Phase Peptide Synthesis*, W. H. Freeman Co., San Francisco, Calif. (1969); Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963)]. In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for

instance, using an Applied Biosystems Peptide Synthesizer (Foster City, Calif.) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., *supra*; Dieffenbach et al., *PCR Primer: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P -labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., *supra*.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., *supra*, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: a Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., *supra*.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 Jun. 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Pat. No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 Apr. 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype tonA; *E. coli* W3110 strain 9E4, which has the complete genotype tonA ptr3; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r; *E. coli* W3110 strain 37D6, which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant degP deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Pat. No. 4,946,783 issued 7 Aug. 1990. Alternatively, in vitro methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and

Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Pat. No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *Yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 Oct. 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/000357 published 10 Jan. 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera Sf9*, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal

sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Pat. No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 Apr. 1990), or the signal described in WO 90/13646 published 15 Nov. 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp 1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., *Nature*, 282:39 (1979); Kingsman et al., *Gene*, 7:141 (1979); Tschemper et al., *Gene*, 10:157 (1980)]. The *trp 1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., *Nature*, 275:615 (1978); Goeddel et al., *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such

as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 Jul. 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201 (1980)], dot blotting (DNA analysis), or in situ hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the

duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods in Enzymology*, 182 (1990); Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ³²P or ³⁵S, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/

biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*BioTechniques* 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable in vivo (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO₄-mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either in vivo or ex vivo. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of

the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as in situ hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding

PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock-out animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve in vivo synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes in vivo. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al., *Proc. Natl. Acad. Sci. USA* 83:4143-4146

[1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells in vitro, or in vivo in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells in vitro include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred in vivo gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., J. Biol. Chem. 262, 4429-4432 (1987); and Wagner et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less

than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, PLURONICSTM or PEG.

The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In Toxicokinetics and New Drug Development, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

When in vivo administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon- (rhIFN-), interleukin-2, and MN rgp120. Johnson et al., Nat. Med., 2:795-799 (1996); Yasuda, Biomed. Ther., 27:1221-1223 (1993); Hora et al., Bio/Technology, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using polylactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable

properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), *Biodegradable Polymers as Drug Delivery Systems* (Marcel Dekker: New York, 1990), pp. 1-41.

This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, *Nature* (London), 340:245-246 (1989); Chien et al., *Proc. Natl. Acad. Sci. USA*, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA*, 89: 5789-5793 (1991). Many transcriptional activators, such as

yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-lacZ reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., *Current Protocols in Immun.*, 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and

sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix—see Lee et al., *Nucl. Acids Res.*, 6:3073 (1979); Cooney et al., *Science*, 241: 456 (1988); Dervan et al., *Science*, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the PRO polypeptide (antisense—Okano, *Neurochem.*, 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, Fla., 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not

limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, *Current Biology*, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published Sep. 18, 1997).

Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

F. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line

using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59–103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (“HAT medium”), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, Calif. and the American Type Culture Collection, Manassas, Va. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51–63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown in vivo as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the

coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Pat. No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522–525 (1986); Riechmann et al., *Nature*, 332:323–329 (1988); and Presta, *Curr. Opin. Struct. Biol.*, 2:593–596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as “import” residues, which are typically taken from an “import” variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522–525 (1986); Riechmann et al., *Nature*, 332:323–327 (1988); Verhoeven et al., *Science*, 239:1534–1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such “humanized” antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact

human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86–95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/Technology* 10, 779–783 (1992); Lonberg et al., *Nature* 368 856–859 (1994); Morrison, *Nature* 368, 812–13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845–51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65–93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuellar, *Nature*, 305:537–539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Trautnecker et al., *EMBO J.*, 10:3655–3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired,

the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., *Methods in Enzymology*, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory “cavities” of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan et al., *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217(1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148 (5):1547–1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The “diabody” technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444–6448(1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of

one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., J. Immunol. 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g., CD2, CD3, CD28, or B7), or Fc receptors for IgG (Fc γ R), such as Fc γ RI (CD64), Fc γ RII (CD32) and Fc γ RIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Pat. No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980.

6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al. Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., Anti-Cancer Drug Design, 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used

include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, croton, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomyacin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re . Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azido-benzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al., Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionuclide to the antibody. See WO 94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionuclide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., J. National Cancer Inst., 81(19): 1484 (1989).

9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding

domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., *Proc. Natl. Acad. Sci. USA*, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's *Pharmaceutical Sciences*, supra.

The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37° C., resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S—S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

C. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, e.g., detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp.

147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ³H, ¹⁴C, ³²P, ³⁵S, or ¹²⁵I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, Va.

Example 1

Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g., LIFESEQTM, Incyte Pharmaceuticals, Palo Alto, Calif.). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Wash.).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not

always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100–1000 bp in length. The probe sequences are typically 40–55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1–1.5 kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., *Current Protocols in Molecular Biology*, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, Calif. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to Sall hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278–1280 (1991)) in the unique XhoI and NotI sites.

Example 2

Isolation of cDNA Clones by Amylase Screening

1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, Calif. (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, Md. (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the Sall/NotI linked cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500–1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37° C. for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37° C.). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in sec 71, sec 72, sec 62, with truncated sec 71 being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz et al., *Nucl. Acid. Res.*, 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30° C. The YEPD broth was prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 207 (1994). The overnight culture was then diluted to about 2×10⁶ cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10⁷ cells/ml (approx. OD₆₀₀=0.4–0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, Md.) and transforming DNA (1 µg, vol. <10 µl) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 µl, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30° C. while agitating for 30 minutes. The cells were then heat shocked at 42° C. for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5–10 seconds, decanted and resuspended into TE (500 µl, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted

into TE (1 ml) and aliquots (200 µl) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 208–210 (1994). Transformants were grown at 30° C. for 2–3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al., *Anal. Biochem.*, 172:176–179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50–100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 µl) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 µl) was used as a template for the PCR reaction in a 25 µl volume containing: 0.5 µl Klentaq (Clontech, Palo Alto, Calif.); 4.0 µl 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 µl Kentaq buffer (Clontech); 0.25 µl forward oligo 1; 0.25 µl reverse oligo 2; 12.5 µl distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACGACGGCCAGTTAAATAGAC-CTGCAATTATTAATCT-3' (SEQ ID NO:169)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACAC-CTGCAAATCCATT-3' (SEQ ID NO:170)

PCR was then performed as follows:

a.		Denature	92° C.,	5 minutes
b.	3 cycles of:	Denature	92° C.,	30 seconds
		Anneal	59° C.,	30 seconds
		Extend	72° C.,	60 seconds
c.	3 cycles of:	Denature	92° C.,	30 seconds
		Anneal	57° C.,	30 seconds
		Extend	72° C.,	60 seconds
d.	25 cycles of:	Denature	92° C.,	30 seconds
		Anneal	55° C.,	30 seconds
		Extend	72° C.,	60 seconds
e.		Hold	4° C.	

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343

bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 µl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, Calif.).

Example 3

Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, Calif.) upon ESTs as well as clustered and assembled EST fragments from public (e.g., GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, Calif.) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

Example 4

Isolation of cDNA Clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209, USA (ATCC) as shown in Tabl 7 below.

TABLE 7

Material	ATCC Dep. No.	Deposit Date
DNA26843-1389	203099	Aug. 4,1998
DNA30867-1335	209807	Apr. 28, 1998
DNA34431-1177	209399	Oct. 17, 1997
DNA38268-1188	209421	Oct. 28, 1997
DNA40621-1440	209922	Jun. 2, 1998
DNA40625-1189	209788	Apr. 21, 1998
DNA45409-2511	203579	Jan. 12,1999
DNA45495-1550	203156	Aug. 25, 1998
DNA49820-1427	209932	Jun. 2, 1998
DNA56406-1704	203478	Nov. 17, 1998
DNA56410-1414	209923	Jun. 2, 1998
DNA56436-1448	209902	May 27, 1998
DNA56855-1447	203004	Jun. 23, 1998
DNA56860-1510	209952	Jun. 9, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA56862-1343	203174	Sep. 1, 1998
DNA56868-1478	203024	Jun. 23, 1998
DNA56869-1545	203161	Aug. 25, 1998
DNA57704-1452	209953	Jun. 9, 1998
DNA58723-1588	203133	Aug. 18, 1998
DNA57827-1493	203045	Jul. 1, 1998
DNA58737-1473	203136	Aug. 18, 1998
DNA58846-1409	209957	Jun. 9, 1998
DNA58850-1495	209956	Jun. 9, 1998
DNA58855-1422	203018	Jun. 23, 1998
DNA59211-1450	209960	Jun. 9, 1998
DNA59212-1627	203245	Sep. 9, 1998
DNA59213-1487	209959	Jun. 9, 1998
DNA59605-1418	203005	Jun. 23, 1998
DNA59609-1470	209963	Jun. 9, 1998
DNA59610-1556	209990	Jun. 16, 1998
DNA59837-2545	203658	Feb. 9, 1999
DNA59844-2542	203650	Feb. 9, 1999
DNA59854-1459	209974	Jun. 16, 1998
DNA60625-1507	209975	Jun. 16, 1998
DNA60629-1481	209979	Jun. 16, 1998
DNA61755-1554	203112	Aug. 11, 1998
DNA62812-1594	203248	Sep. 9, 1998
DNA62815-1576	203247	Sep. 9, 1998
DNA64881-1602	203240	Sep. 9, 1998
DNA64886-1601	203241	Sep. 9, 1998
DNA64902-1667	203317	Oct. 6, 1998
DNA64950-1590	203224	Sep. 15, 1998
DNA65403-1565	203230	Sep. 15, 1998
DNA66308-1537	203159	Aug. 25, 1998
DNA66519-1535	203236	Sep. 15, 1998
DNA66521-1583	203225	Sep. 15, 1998
DNA66658-1584	203229	Sep. 15, 1998
DNA66660-1585	203279	Sep. 22, 1998
DNA66663-1598	203268	Sep. 22, 1998
DNA66674-1599	203281	Sep. 22, 1998
DNA68862-2546	203652	Feb. 9, 1999
DNA68866-1644	203283	Sep. 22, 1998
DNA68871-1638	203280	Sep. 22, 1998
DNA68880-1676	203319	Oct. 6, 1998
DNA68883-1691	203535	Dec. 15, 1998
DNA68885-1678	203311	Oct. 6, 1998
DNA71277-1636	203285	Sep. 22, 1998
DNA73727-1673	203459	Nov. 3, 1998
DNA73734-1680	203363	Oct. 20, 1998
DNA73735-1681	203356	Oct. 20, 1998
DNA76393-1664	203323	Oct. 6, 1998
DNA77301-1708	203407	Oct. 27, 1998
DNA77568-1626	203134	Aug. 18, 1998
DNA77626-1705	203536	Dec. 15, 1998
DNA81754-2532	203542	Dec. 15, 1998
DNA81757-2512	203543	Dec. 15, 1998
DNA82302-2529	203534	Dec. 15, 1998
DNA82340-2530	203547	Dec. 22, 1998
DNA83500-2506	203391	Oct. 29, 1998
DNA84920-2614	203966	Apr. 27, 1999
DNA85066-2534	203588	Jan. 12, 1999
DNA86571-2551	203660	Feb. 9, 1999
DNA87991-2540	203656	Feb. 9, 1999
DNA92238-2539	203602	Jan. 20, 1999
DNA96042-2682	PTA-382	Jul. 20, 1999
DNA96787-2534	203589	Jan. 12, 1999
DNA125185-2806	PTA-1031	Dec. 7, 1999
DNA147531-2821	PTA-1185	Jan. 11, 2000
DNA115291-2681	PTA-202	Jun. 8, 1999
DNA164625-28890	PTA-1535	Mar. 21, 2000
DNA131639-2874	PTA-1784	Apr. 25, 2000
DNA79230-2525	203549	Dec. 22, 1998

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be

made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

Example 5

Use of PRO as a Hybridization Probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5×SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2× Denhardt's solution, and 10% dextran sulfate at 42° C. for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1×SSC and 0.1% SDS at 42° C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

Example 6

Expression of PRO in *E. Coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et

al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) Ion galE rpoHts (htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30° C. with shaking until an O.D.600 of 3–5 is reached. Cultures are then diluted 50–100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate-2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20–30 hours at 30° C. with shaking. Samples are removed to verify expression by SDS-page analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6–10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4° C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3–5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4° C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4° C. for 12–36 hours. The refolding reaction is

quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2–10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 7

Expression of PRO in Mammalian Cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published Mar. 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-PRO DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25° C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37° C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml ³⁵S-cysteine and 200 µCi/ml ³⁵S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may

undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24:9 (1774-1779 (1996)), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Qiagen), Dosper® or Eugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., *supra*. Approximately 3×10^{-7} cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μ m filtered PS20 with 5% 0.2 μ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37° C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Pat. No. 5,122,469, issued Jun. 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33° C., and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μ m filter. The filtrate was either stored at 4° C. or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4° C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80° C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 9

Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4–5 days of incubation at 28° C., the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175–179 (1993). Briefly, Sf9 cells are washed, resuspended in soni-

cation buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 10

Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1–100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, Mont.) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

113

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

Example 11

Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2–3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

Example 12

Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids

114

expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with a PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on Sep. 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

Example 13

Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (i.e., a PRO polypeptide) or of small molecules with which they interact, e.g., agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide in vivo (c.f., Hodgson, *Bio/Technology*, 9: 19–21(1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of a PRO polypeptide-inhibitor complex, is determined by X-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO

115

polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda et al., *J. Biochem.*, 113: 742-746(1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to X-ray crystallography.

Example 14

Pericyte c-Fos Induction (Assay 93)

This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Induction of c-fos expression in pericytes is also indicative of the induction of angiogenesis and, as such, PRO polypeptides capable of inducing the expression of c-fos would be expected to be useful for the treatment of conditions where induced angiogenesis would be beneficial including, for example, wound healing, and the like. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100 μ l of PRO polypeptide test samples and controls (positive control=DME+5% serum+/-PDGF at 500 ng/ml; negative control=protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media=low glucose DMEM=20% FBS+1 $\times$ pen strep+1 $\times$ fungizone. Assay Media=low glucose DMEM+5% FBS.

The following polypeptides tested positive in this assay: PRO1347 and PRO1340.

Example 15

Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)

The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

116

The metacarpophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% CO₂ in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100 U/ml penicillin and 100 μ g/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into microtubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 18 ng/ml interleukin-1 α , a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, *Biochem. Biophys. Acta* 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1 α and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. The polypeptides testing positive in this assay are: PRO1565, PRO1693, PRO1801 and PRO10096.

Example 16

Detection of Polypeptides that Affect Glucose or FFA Uptake in Skeletal Muscle (Assay 106)

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by skeletal muscle cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by skeletal muscle would be beneficial including, for example, diabetes or hyper- or hypo-insulinemia.

In a 96 well format, PRO polypeptides to be assayed are added to primary rat differentiated skeletal muscle, and allowed to incubate overnight. Then fresh media with the PRO polypeptide and +/- insulin are added to the wells. The sample media is then monitored to determine glucose and FFA uptake by the skeletal muscle cells. The insulin will stimulate glucose and FFA uptake by the skeletal muscle, and insulin in media without the PRO polypeptide is used as a positive control, and a limit for scoring. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as either stimulators or inhibitors of glucose and/or FFA uptake in this assay: PRO4405.

Example 17

Identification of PRO Polypeptides that Stimulate TNF- α Release in Human Blood (Assay 128)

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- α in human blood. PRO polypeptides testing positive in this

assay are useful for, among other things, research purposes where stimulation of the release of TNF- α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- α release would be beneficial. Specifically, 200 μ l of human blood supplemented with 50 mM Hepes buffer (pH 7.2) is aliquotted per well in a 96 well test plate. To each well is then added 300 μ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37° C. for 6 hours. The samples are then centrifuged and 50 μ l of plasma is collected from each well and tested for the presence of TNF- α by ELISA assay. A positive in the assay is a higher amount of TNF- α in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay: PRO263, PRO295, PRO1282, PRO1063, PRO1356, PRO3543, and PRO5990.

Example 18

Tumor Versus Normal Differential Tissue Expression Distribution

Oligonucleotide probes were constructed from some of the PRO polypeptide-encoding nucleotide sequences shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200–600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human tumor and normal human tissue samples and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tumor and normal tissues tested. β -actin was used as a control to assure that equivalent amounts of nucleic acid was used in each reaction. Identification of the differential expression of the PRO polypeptide-encoding nucleic acid in one or more tumor tissues as compared to one or more normal tissues of the same tissue type renders the molecule useful diagnostically for the determination of the presence or absence of tumor in a subject suspected of possessing a tumor as well as therapeutically as a target for the treatment of a tumor in a subject possessing such a tumor. These assays provided the following results.

Molecule	is more highly expressed in:	as compared to:
DNA26843-1389	normal lung	lung tumor
	rectum tumor	normal rectum
DNA30867-1335	normal kidney	kidney tumor
DNA40621-1440	normal lung	lung tumor
DNA40625-1189	normal lung	lung tumor
DNA45409-2511	melanoma tumor	normal skin
DNA56406-1704	kidney tumor	normal kidney
	normal skin	melanoma tumor
DNA56410-1414	normal stomach	stomach tumor
DNA56436-1448	normal skin	melanoma tumor
DNA56855-1447	normal esophagus	esophageal tumor
	rectum tumor	normal rectum
DNA56860-1510	normal kidney	kidney tumor
	rectum tumor	normal rectum
DNA56862-1343	kidney tumor	normal kidney
	normal lung	lung tumor
DNA56868-1478	normal stomach	stomach tumor
	normal lung	lung tumor
DNA56869-1545	normal esophagus	esophageal tumor
	normal skin	melanoma tumor

-continued

Molecule	is more highly expressed in:	as compared to:
5 DNA57704-1452	normal stomach	stomach tumor
	rectum tumor	normal rectum
DNA58723-1588	normal stomach	stomach tumor
	kidney tumor	normal kidney
	normal skin	melanoma tumor
DNA57827-1493	normal stomach	stomach tumor
10 DNA58737-1473	normal skin	melanoma tumor
	esophageal tumor	normal esophagus
	normal stomach	stomach tumor
DNA58846-1409	lung tumor	normal lung
DNA58850-1495	esophageal tumor	normal esophagus
	kidney tumor	normal kidney
15 DNA58855-1422	normal stomach	stomach tumor
	rectum tumor	normal rectum
DNA59211-1450	normal kidney	kidney tumor
DNA59212-1627	normal skin	melanoma tumor
DNA59213-1487	normal stomach	stomach tumor
	normal skin	melanoma tumor
20 DNA59605-1418	melanoma tumor	normal skin
DNA59609-1470	esophageal tumor	normal esophagus
DNA59610-1556	esophageal tumor	normal esophagus
	lung tumor	normal lung
	normal skin	melanoma tumor
DNA59837-2545	normal skin	melanoma tumor
DNA59844-2542	normal skin	melanoma tumor
25 DNA59854-1459	esophageal tumor	normal esophagus
	normal esophagus	esophageal tumor
	stomach tumor	normal stomach
	normal lung	lung tumor
DNA60625-1507	normal lung	lung tumor
DNA60629-1481	normal esophagus	esophageal tumor
30 DNA61755-1554	normal rectum	rectum tumor
	normal stomach	stomach tumor
	kidney tumor	normal kidney
DNA62812-1594	normal stomach	stomach tumor
	normal lung	lung tumor
	normal rectum	rectum tumor
35 DNA62815-1576	normal skin	melanoma tumor
DNA64881-1602	esophageal tumor	normal esophagus
	normal stomach	stomach tumor
	normal lung	lung tumor
DNA64902-1667	esophageal tumor	normal esophagus
	kidney tumor	normal kidney
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DNA66308-1537	normal lung	lung tumor
DNA66519-1535	kidney tumor	normal kidney
DNA66521-1583	normal esophagus	esophageal tumor
	normal stomach	stomach tumor
	normal lung	lung tumor
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	normal skin	melanoma tumor
	normal lung	lung tumor
	melanoma tumor	normal skin
DNA66660-1585	lung tumor	normal lung
DNA66674-1599	kidney tumor	normal kidney
	normal lung	lung tumor
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DNA68866-1644	normal stomach	stomach tumor
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	normal skin	melanoma tumor
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	normal skin	melanoma tumor
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DNA71277-1636	normal stomach	stomach tumor
DNA73734-1680	normal lung	lung tumor
DNA73735-1681	esophageal tumor	normal esophagus
	normal kidney	kidney tumor
60 DNA76393-1664	lung tumor	normal lung
	normal skin	melanoma tumor
	esophageal tumor	normal esophagus
	stomach tumor	normal stomach
	lung tumor	normal lung
	rectum tumor	normal rectum
DNA77568-1626	normal stomach	stomach tumor
65 DNA77626-1705	lung tumor	normal lung
	normal rectum	rectum tumor

-continued

Molecule	is more highly expressed in:	as compared to:
DNA81754-2532	normal skin	melanoma tumor
DNA81757-2512	esophageal tumor	normal esophagus
	normal stomach	stomach tumor
	melanoma tumor	normal skin
DNA82302-2529	normal stomach	stomach tumor
	normal lung	lung tumor
DNA82340-2530	normal esophagus	esophageal tumor
DNA85066-2534	lung tumor	normal lung
	normal skin	melanoma tumor
DNA87991-2540	esophageal tumor	normal esophagus
DNA92238-2539	normal skin	melanoma tumor
DNA96787-2534	normal kidney	kidney tumor

Example 19

Identification of Receptor/Ligand Interactions

In this assay, various PRO polypeptides are tested for ability to bind to a panel of potential receptor or ligand molecules for the purpose of identifying receptor/ligand interactions. The identification of a ligand for a known receptor, a receptor for a known ligand or a novel receptor/ligand pair is useful for a variety of indications including, for example, targeting bioactive molecules (linked to the ligand or receptor) to a cell known to express the receptor or ligand, use of the receptor or ligand as a reagent to detect the presence of the ligand or receptor in a composition suspected of containing the same, wherein the composition may comprise cells suspected of expressing the ligand or receptor, modulating the growth of or another biological or immunological activity of a cell known to express or respond to the receptor or ligand, modulating the immune response of cells or toward cells that express the receptor or ligand, allowing the preparation of agonists, antagonists and/or antibodies directed against the receptor or ligand which will modulate the growth of or a biological or immunological activity of a cell expressing the receptor or ligand, and various other indications which will be readily apparent to the ordinarily skilled artisan.

The assay is performed as follows. A PRO polypeptide of the present invention suspected of being a ligand for a receptor is expressed as a fusion protein containing the Fc domain of human IgG (an immunoadhesin). Receptor-ligand binding is detected by allowing interaction of the immunoadhesin polypeptide with cells (e.g. Cos cells) expressing candidate PRO polypeptide receptors and visualization of bound immunoadhesin with fluorescent reagents directed toward the Fc fusion domain and examination by microscope. Cells expressing candidate receptors are produced by transient transfection, in parallel, of defined subsets of a library of cDNA expression vectors encoding PRO polypeptides that may function as receptor molecules. Cells are then incubated for 1 hour in the presence of the PRO polypeptide immunoadhesin being tested for possible receptor binding.

The cells are then washed and fixed with paraformaldehyde. The cells are then incubated with fluorescent conjugated antibody directed against the Fc portion of the PRO polypeptide immunoadhesin (e.g. FITC conjugated goat anti-human-Fc antibody). The cells are then washed again and examined by microscope. A positive interaction is judged by the presence of fluorescent labeling of cells transfected with cDNA encoding a particular PRO polypeptide receptor or pool of receptors and an absence of similar fluorescent labeling of similarly prepared cells that have been transfected with other cDNA or pools of cDNA. If a defined pool of cDNA expression vectors is judged to be positive for interaction with a PRO polypeptide immunoadhesin, the individual cDNA species that comprise the pool are tested individually (the pool is "broken down") to determine the specific cDNA that encodes a receptor able to interact with the PRO polypeptide immunoadhesin.

In another embodiment of this assay, an epitope-tagged potential ligand PRO polypeptide (e.g. 8 histidine "His" tag) is allowed to interact with a panel of potential receptor PRO polypeptide molecules that have been expressed as fusions with the Fc domain of human IgG (immunoadhesins). Following a 1 hour co-incubation with the epitope tagged PRO polypeptide, the candidate receptors are each immunoprecipitated with protein A beads and the beads are washed. Potential ligand interaction is determined by western blot analysis of the immunoprecipitated complexes with antibody directed towards the epitope tag. An interaction is judged to occur if a band of the anticipated molecular weight of the epitope tagged protein is observed in the western blot analysis with a candidate receptor, but is not observed to occur with the other members of the panel of potential receptors.

Using these assays, the following receptor/ligand interactions have been herein identified:

(1) PRO10272 binds to PRO5801.

(2) PRO20110 binds to the human IL-17 receptor (Yao et al., *Cytokine* 9(11):794-800 (1997); also herein designated as PRO1) and to PRO20040.

(3) PRO10096 binds to PRO20233.

(4) PRO19670 binds to PRO1890.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

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Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val	
80 85 90	
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu	
95 100 105	
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe	
110 115 120	
Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser	
125 130 135	

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Pro Lys His Gly	Ile Leu Ser Ile Glu	Gln Leu Ile Ser Arg Val
140		145 150
Gly Val Ile Gly	Val Thr Leu Met Ala	Leu Leu Ser Gly Phe Gly
155		160 165
Ala Val Asn Cys	Pro Tyr Thr Tyr Met	Ser Tyr Phe Leu Arg Asn
170		175 180
Val Thr Asp Thr	Asp Ile Leu Ala Leu	Glu Arg Arg Leu Leu Gln
185		190 195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met Ala
200		205 210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro Ser
215		220 225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser Gly
230		235 240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu Glu
245		250 255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr Ala
260		265 270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys Tyr
275		280 285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp Lys
290		295 300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly Lys
305		310 315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr Leu
320		325 330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser Phe
335		340 345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu Leu
350		355 360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys Ser
365		370 375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met Tyr
380		385 390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu Glu
395		400 405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe Asn
410		415 420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala Leu
425		430 435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro Glu
440		445 450
Lys Gln Met Ala	Pro	
455		

<210> SEQ ID NO 5

<211> LENGTH: 2372

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 5

agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag

50

cctcaacata gttccagaac tctccatccg gactagttat tgagcatctg

100

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cctctcatat caccagtggc catctgaggt gtttccctgg ctctgaagg	150
gtaggcacga tggccagggt cttcagcctg gtgttgcttc tcacttccat	200
ctggaccacg aggtcctctg tccaaggctc tttgcgtgca gaagagcttt	250
ccatccagggt gtcatgcaga attatgggga tcacccttgt gagcaaaaag	300
gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct	350
gggactaagt ttggccggca aggaccaagt tgaacagcc ttgaaagcta	400
gctttgaaac ttgcagctat ggctgggttg gagatggatt cgtggtcac	450
tctaggatta gccc aaaccc caagtgtggg aaaaatggg tgggtgtcct	500
gatttggaag gttccagtga gccgacagtt tgcagcctat tgttacaact	550
catctgatac ttggactaac tcgtgcattc cagaaattat caccaccaa	600
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt	650
cagtgcagct acctactcgg tggcatcccc ttactctaca atacctgcc	700
ctactactac tcctcctgct ccagcttcca cttctattcc acggagaaaa	750
aaattgattt gtgtcacaga agtttttatg gaaactagca ccatgtctac	800
agaaactgaa ccatttgttg aaaataaagc agcattcaag aatgaagctg	850
ctgggttttg aggtgtcccc acggctctgc tagtgcttgc tctcctcttc	900
tttgggtgctg cagctgggtct tggattttgc tatgtcaaaa ggtatgtgaa	950
ggccttccct ttacaaaca agaatacagca gaaggaaatg atcgaaacca	1000
aagtagtaaa ggaggagaag gccaatgata gcaaccctaa tgaggaaatca	1050
aagaaaactg ataaaaaccc agaagagtcc aagagtccaa gcaaaactac	1100
cgtgcgatgc ctggaagctg aagtttagat gagacagaaa tgaggagaca	1150
cacctgaggc tgggtttctt catgtctctt accctgcccc agctggggaa	1200
atcaaaaggg ccaaagaacc aaagaagaaa gtccaccctt ggttcctaac	1250
tggaatcagc tcaggactgc cattggacta tggagtgcac caaagagaat	1300
gcccttcttc ttattgtaac cctgtctgga tcctatcttc ctacctcaa	1350
agcttccac gccctttcta gcctggctat gtcctaataa tatccactg	1400
ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc tcatcagtat	1450
ccagtggtaa aaaggcctcc tggctgtctg aggtctagtg ggttgaaagc	1500
caaggagtca ctgagaccaa ggctttctct actgattccg cagctcagac	1550
cctttcttca gctctgaaag agaaacacgt atcccacctg acatgtcctt	1600
ctgagcccg taagagcaaa agaattggcag aaaagtttag cccctgaaag	1650
ccatggagat tctcataact tgagacctaa tctctgtaaa gctaaaataa	1700
agaaatagaa caaggctgag gatacgacag tacactgtca gcagggactg	1750
taaacacaga cagggtcaaa gtgttttctc tgaacacatt gagttggaat	1800
cactgtttag aacacacaca cttacttttt ctggtctcta ccactgctga	1850
tattttctct aggaaatata cttttacaag taacaaaaat aaaaactctt	1900
ataaatttct atttttatct gagttacaga aatgattact aaggaagatt	1950
actcagtaat ttgttttaaa agtaataaaa ttcaacaaac atttgctgaa	2000
tagctactat atgtcaagt ctgtgcaagg tattacactc tgtaattgaa	2050
tattattcct caaaaaattg cacatagtag aacgctatct ggaagctat	2100

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ttttttcagt ttgatattt ctagcttata tacttcctaaa ctaattttta      2150
tttttgctga gactaatctt attcattttc tctaataatgg caaccattat      2200
aaccttaatt tattattaac atacctaaga agtacattgt tacctctata      2250
taccaaagca catttttaaaa gtgccattaa caaatgtatc actagccctc      2300
ctttttccaa caagaaggga ctgagagatg cagaaatatt tgtgacaaaa      2350
aattaaagca tttagaaaac tt                                     2372

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<210> SEQ ID NO 6
<211> LENGTH: 322
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 6

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Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp
  1             5             10             15
Thr Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu
 20             25             30
Ser Ile Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser
 35             40             45
Lys Lys Ala Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala
 50             55             60
Cys Arg Leu Leu Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu
 65             70             75
Thr Ala Leu Lys Ala Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val
 80             85             90
Gly Asp Gly Phe Val Val Ile Ser Arg Ile Ser Pro Asn Pro Lys
 95            100            105
Cys Gly Lys Asn Gly Val Gly Val Leu Ile Trp Lys Val Pro Val
110            115            120
Ser Arg Gln Phe Ala Ala Tyr Cys Tyr Asn Ser Ser Asp Thr Trp
125            130            135
Thr Asn Ser Cys Ile Pro Glu Ile Ile Thr Thr Lys Asp Pro Ile
140            145            150
Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr Glu Phe Ile Val Ser
155            160            165
Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser Thr Ile Pro Ala
170            175            180
Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser Ile Pro Arg
185            190            195
Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu Thr Ser
200            205            210
Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala Ala
215            220            225
Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
230            235            240
Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly
245            250            255
Phe Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn
260            265            270
Lys Asn Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu
275            280            285
Glu Lys Ala Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr

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	290	295	300	
Asp Lys Asn Pro Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val				
	305	310	315	
Arg Cys Leu Glu Ala Glu Val				
	320			
 <210> SEQ ID NO 7				
<211> LENGTH: 2586				
<212> TYPE: DNA				
<213> ORGANISM: Homo Sapien				
 <400> SEQUENCE: 7				
cgccgcgctc ccgcacccgc ggcccgccca ccgcgcgcgt cccgcattctg				50
caccgcgcagc ccggcggcct cccggcggga gcgagcagat ccagtcgggc				100
ccgcagcgca actcgggtcca gtcggggcgg cggtgcggg cgcagagcgg				150
agatgcagcg gcttggggcc accctgctgt gcctgctgct ggcggcggcg				200
gtccccacgg ccccccgcgc cgctccgacg gcgacctcgg ctccagtcaa				250
gcccggcccc gctctcagct acccgcagga ggaggccacc ctcaatgaga				300
tgttccgcga ggttgaggaa ctgatggagg acacgcagca caaattgcgc				350
agcgcggtgg aagagatgga ggcagaagaa gctgctgcta aagcatcatc				400
agaagtgaac ctggcaaaact tacctcccag ctatcacaaat gagaccaaca				450
cagacacgaa ggttggaat aataccatcc atgtgcaccg agaaattcac				500
aagataacca acaaccagac tggacaaatg gtcttttcag agacagttat				550
cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcattcatcg				600
acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac				650
acctgccagc catgccgggg ccagaggatg ctctgcaccc gggacagtga				700
gtgctgtgga gaccagctgt gtgtctgggg tcaactgcacc aaaatggcca				750
ccaggggcag caatgggacc atctgtgaca accagaggga ctgccagccg				800
gggtgtgct gtgccttcca gagaggcctg ctgttccctg tgtgcacacc				850
cctgcccgtg gagggcgagc tttgccatga cccgcgcagc cggcttcttg				900
acctcatcac ctgggagcta gagcctgatg gagccttga ccgatgcctt				950
tgtgccagtg gcctcctctg ccagccccc agccacagcc tgggtgatgt				1000
gtgcaagccg accttcgtgg ggagccgtga ccaagatggg gagatcctgc				1050
tgcccagaga ggtccccgat gagtatgaag ttggcagctt catggaggag				1100
gtgcgccagg agctggagga cctggagagg agcctgactg aagagatggc				1150
gctgggggag cctgcggctg ccgccgctgc actgctggga ggggaagaga				1200
tttagatctg gaccaggctg tgggtagatg tgcaatagaa atagctaatt				1250
tatttcccca ggtgtgtgct ttaggcgtgg gctgaccagg cttcttccta				1300
catcttcttc ccagtaagtt tcccctctgg cttgacagca tgagggtgtg				1350
tgcatattgt cagctcccc aggtgtttct ccaggcttca cagtctggtg				1400
cttgggagag tcaggcaggg ttaaactgca ggagcagttt gccacccctg				1450
tccagattat tggctgcttt gcctctacca gttggcagac agccgtttgt				1500
tctacatggc ttgataaatt gtttgagggg aggagatgga aacaatgtgg				1550
agtctccctc tgattggttt tggggaaatg tggagaagag tgccttgcct				1600

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tgcaaacatc aacctggcaa aaatgcaaca aatgaatttt ccacgcagtt	1650
ctttccatgg gcataggtaa gctgtgcctt cagctgttgc agatgaaatg	1700
ttctgttcac cctgcattac atgtgtttat tcatccagca gtgttgctca	1750
gctectacct ctgtgccagg gcagcatttt catatccaag atcaattccc	1800
tctctcagca cagcctgggg agggggtcat tgttctcttc gtccatcagg	1850
gatctcagag gctcagagac tgcaagctgc ttgcccaagt cacacageta	1900
gtgaagacca gagcagtttc atctggttgt gactctaagc tcagtgtctt	1950
ctccactacc ccacaccagc cttggtgccca ccaaaagtgc tccccaaaag	2000
gaaggagaat gggatttttc ttgaggcatg cacatctgga attaaggtca	2050
aactaattct cacatccctc taaaagtaaa ctactgttag gaacagcagt	2100
gttctcacag tgtggggcag ccgtccttct aatgaagaca atgatattga	2150
cactgtccct ctttggcagt tgcattagta actttgaaag gtatatgact	2200
gagcgtagca tacaggttaa cctgcagaaa cagtacttag gtaattgtag	2250
ggcgaggatt ataaatgaaa ttgcaaaaat cacttagcag caactgaaga	2300
caattatcaa ccacgtggag aaaatcaaac cgagcagggc tgtgtgaaac	2350
atggttgtaa tatgcgactg cgaacactga actctacgcc actccacaaa	2400
tgatgttttc aggtgtcatg gactgttgcc accatgtatt catccagagt	2450
tcttaaagtt taaagttgca catgattgta taagcatgct ttctttgagt	2500
tttaaattat gtataaacat aagttgcatt tagaaatcaa gcataaatca	2550
cttcaactgc aaaaaaaaaa aaaaaaaaaa aaaaaa	2586

<210> SEQ ID NO 8

<211> LENGTH: 350

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 8

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Ala Ala	
1 5 10 15	
Ala Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala	
20 25 30	
Pro Val Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala	
35 40 45	
Thr Leu Asn Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp	
50 55 60	
Thr Gln His Lys Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu	
65 70 75	
Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn Leu Ala Asn Leu	
80 85 90	
Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr Lys Val Gly	
95 100 105	
Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile Thr Asn	
110 115 120	
Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr Ser	
125 130 135	
Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
140 145 150	

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Glu	Asp	Cys	Gly	Pro	Ser	Met	Tyr	Cys	Gln	Phe	Ala	Ser	Phe	Gln
				155					160					165
Tyr	Thr	Cys	Gln	Pro	Cys	Arg	Gly	Gln	Arg	Met	Leu	Cys	Thr	Arg
				170					175					180
Asp	Ser	Glu	Cys	Cys	Gly	Asp	Gln	Leu	Cys	Val	Trp	Gly	His	Cys
				185					190					195
Thr	Lys	Met	Ala	Thr	Arg	Gly	Ser	Asn	Gly	Thr	Ile	Cys	Asp	Asn
				200					205					210
Gln	Arg	Asp	Cys	Gln	Pro	Gly	Leu	Cys	Cys	Ala	Phe	Gln	Arg	Gly
				215					220					225
Leu	Leu	Phe	Pro	Val	Cys	Thr	Pro	Leu	Pro	Val	Glu	Gly	Glu	Leu
				230					235					240
Cys	His	Asp	Pro	Ala	Ser	Arg	Leu	Leu	Asp	Leu	Ile	Thr	Trp	Glu
				245					250					255
Leu	Glu	Pro	Asp	Gly	Ala	Leu	Asp	Arg	Cys	Pro	Cys	Ala	Ser	Gly
				260					265					270
Leu	Leu	Cys	Gln	Pro	His	Ser	His	Ser	Leu	Val	Tyr	Val	Cys	Lys
				275					280					285
Pro	Thr	Phe	Val	Gly	Ser	Arg	Asp	Gln	Asp	Gly	Glu	Ile	Leu	Leu
				290					295					300
Pro	Arg	Glu	Val	Pro	Asp	Glu	Tyr	Glu	Val	Gly	Ser	Phe	Met	Glu
				305					310					315
Glu	Val	Arg	Gln	Glu	Leu	Glu	Asp	Leu	Glu	Arg	Ser	Leu	Thr	Glu
				320					325					330
Glu	Met	Ala	Leu	Gly	Glu	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu
				335					340					345
Gly	Gly	Glu	Glu	Ile										
				350										

<210> SEQ ID NO 9

<211> LENGTH: 1395

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 9

cggacgcgtg ggcggacgcg tgggggctgt gagaaagtgc caataaatac	50
atcatgcaac cccacggccc accttgtgaa ctccctcgtgc ccagggtga	100
tgtagctctt ccagggtac tcatccaaag gcctaatacca acgttctgtc	150
ttcaatctgc aaatctatgg ggtcctgggg ctcttctgga cccttaactg	200
ggtactggcc ctgggccaat gcgtcctcgc tggagccttt gcctccttct	250
actgggcctt ccacaagccc caggacatcc ctaccttccc cttaatctct	300
gccttcatcc gcacactccg ttaccacact gggtcattgg catttgagc	350
cctcatcctg acccttgtgc agatagcccg ggtcatcttg gagtatatgt	400
accacaagct cagaggagtg cagaacctg tagcccgctg catcatgtgc	450
tgtttcaagt gctgcctctg gtgtctgaa aaatttatca agttcctaaa	500
ccgcaatgca tacatcatga tcgccatcta cggaagaat ttctgtgtct	550
cagccaaaaa tgcgttcattg ctactcatgc gaaacattgt cagggtgggc	600
gtcctggaca aagtcacaga cctgtgtctg ttctttggga agctgtgtgt	650
ggtcggaggc gtgggggtcc tgtccttctt ttttttctcc ggtcgcaccc	700
cggggtgtgg taaagacttt aagagccccc acctcaacta ttactggctg	750

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cccatcatga cctccatcct gggggcctat gtcacgcga gcggcttctt      800
cagcggttttc ggcattgtgt tggacacgct cttcctctgc ttcctggaag      850
acctggagcg gaacaacggc tccctggacc ggccctacta catgtccaag      900
agccttctaa agattctggg caagaagaac gaggcgcccc cggacaacaa      950
gaagaggaag aagtgcacgc tccggccctg atccaggact gcacccacc      1000
cccaccgtcc agccatccaa cctcacttcg cttacaggt ctccattttg      1050
tggtaaaaaa aggttttagg ccaggcgccg tggctcacgc ctgtaatcca      1100
acactttgag aggtgagggc gggcgatca cctgagtcag gagttcgaga      1150
ccagcctggc caacatggtg aaacctccgt ctctattaaa aataaaaaa      1200
ttagccgaga gtggtggcat gcacctgtca tcccagctac tcgggaggct      1250
gaggcaggag aatcgcttga acccgggagg cagaggttgc agtgagccga      1300
gatcgcgcca ctgcactcca acctgggtga cagactctgt ctccaaaaca      1350
aaacaaacaa aaaaaagat ttatttaaag atattttgtt aactc      1395

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<210> SEQ ID NO 10

<211> LENGTH: 321

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 10

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Arg Thr Arg Gly Arg Thr Arg Gly Gly Cys Glu Lys Val Pro Ile
  1          5          10          15
Asn Thr Ser Cys Asn Pro Thr Ala His Leu Val Asn Ser Ser Cys
  20          25          30
Pro Gly Leu Met Cys Val Phe Gln Gly Tyr Ser Ser Lys Gly Leu
  35          40          45
Ile Gln Arg Ser Val Phe Asn Leu Gln Ile Tyr Gly Val Leu Gly
  50          55          60
Leu Phe Trp Thr Leu Asn Trp Val Leu Ala Leu Gly Gln Cys Val
  65          70          75
Leu Ala Gly Ala Phe Ala Ser Phe Tyr Trp Ala Phe His Lys Pro
  80          85          90
Gln Asp Ile Pro Thr Phe Pro Leu Ile Ser Ala Phe Ile Arg Thr
  95          100         105
Leu Arg Tyr His Thr Gly Ser Leu Ala Phe Gly Ala Leu Ile Leu
  110         115         120
Thr Leu Val Gln Ile Ala Arg Val Ile Leu Glu Tyr Ile Asp His
  125         130         135
Lys Leu Arg Gly Val Gln Asn Pro Val Ala Arg Cys Ile Met Cys
  140         145         150
Cys Phe Lys Cys Cys Leu Trp Cys Leu Glu Lys Phe Ile Lys Phe
  155         160         165
Leu Asn Arg Asn Ala Tyr Ile Met Ile Ala Ile Tyr Gly Lys Asn
  170         175         180
Phe Cys Val Ser Ala Lys Asn Ala Phe Met Leu Leu Met Arg Asn
  185         190         195
Ile Val Arg Val Val Val Leu Asp Lys Val Thr Asp Leu Leu Leu
  200         205         210
Phe Phe Gly Lys Leu Leu Val Val Gly Gly Val Gly Val Leu Ser
  215         220         225

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Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly Leu Gly Lys Asp Phe
 230 235 240
 Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro Ile Met Thr Ser
 245 250 255
 Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe Ser Val Phe
 260 265 270
 Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu Asp Leu
 275 280 285
 Glu Arg Asn Asn Gly Ser Leu Asp Arg Pro Tyr Tyr Met Ser Lys
 290 295 300
 Ser Leu Leu Lys Ile Leu Gly Lys Lys Asn Glu Ala Pro Pro Asp
 305 310 315
 Asn Lys Lys Arg Lys Lys
 320

<210> SEQ ID NO 11

<211> LENGTH: 1901

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 11

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gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg      100
ctctgcccc tgcatacctgt gcagctgctg ccccgccagc cgcaactcca      150
ccgtgagccg cctcatcttc acgttcttcc tcttctctggg ggtgctggtg      200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc      250
ctgggtgtgt gaggaggggg ccgggatccc caccgtctcg cagggccaca      300
tcgactgtgg ctccctgctt ggetaccgag ctgtctaccg catgtgcttc      350
gccacggcgg ctttcttctt cttctttttc accctgctca tgctctgcgt      400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct      450
ttaagttcct gatcctggtg ggcctcaccg tgggtgcctt ctacatccct      500
gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt      550
cctcttcac ctcataccagc tgggtgctgt catcgacttt gcgcactcct      600
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg      650
tacgcaggcc tcttcttctt cactctcctc ttctacttgc tgtcgatcgc      700
ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg      750
agggcaaggt cttcatcagc ctcaacctca cttctgtgtg ctgcgtgtcc      800
atcgctgctg tcctgccccaa ggtccaggac gccagccca actcgggtct      850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag      900
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag      950
ctgggcaacg agacagtgtg ggcaggcccc gagggctatg agaccagtg      1000
gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc      1050
tcttcatcag tctgcgtccc tcagaccacc ggcaggtgaa cagcctgatg      1100
cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca      1150
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg      1200
tcacctacag ctactccttc ttccacttct gcctggtgct ggcctcactg      1250

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cacgtcatga tgacgtcac caactggtac aagcccgtg agaccggaa      1300
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg      1350
cagggctgct cctctacctg tggaccctgg tagccccact cctcctgcgc      1400
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggcgcctcc      1450
tgccacctgg tgccctctcg ctcggtgaca gccaacctgc cccctcccca      1500
caccaatcag ccaggctgag cccccacccc tgcccagct ccaggacctg      1550
cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat      1600
cagggctcctg cagagcccca tcccccgcc acaccacac ggtggagctg      1650
cctcttcctt cccctcctcc ctgttgccca tactcagcat ctcggatgaa      1700
agggctccct tgcctcagg ctccacggga gcggggctgc tggagagagc      1750
ggggaactcc caccacagt gggcatccgg cactgaagcc ctggtgttcc      1800
tggtcacgtc cccaggggga ccctgcccc ttcctggact tcgtgcctta      1850
ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa      1900
a                                                                1901

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<210> SEQ ID NO 12
<211> LENGTH: 457
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 12

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Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
 1           5           10          15
Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20          25          30
Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35          40          45
Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50          55          60
Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
 65          70          75
Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
 80          85          90
Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
 95          100         105
Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
 110         115         120
Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe
 125         130         135
Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
 140         145         150
Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
 155         160         165
Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
 170         175         180
Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu
 185         190         195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr
 200         205         210

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Leu Leu Phe Tyr	Leu Leu Ser Ile Ala	Ala Val Ala Leu Met Phe
	215	220 225
Met Tyr Tyr Thr	Glu Pro Ser Gly Cys	His Glu Gly Lys Val Phe
	230	235 240
Ile Ser Leu Asn	Leu Thr Phe Cys Val	Cys Val Ser Ile Ala Ala
	245	250 255
Val Leu Pro Lys	Val Gln Asp Ala Gln	Pro Asn Ser Gly Leu Leu
	260	265 270
Gln Ala Ser Val	Ile Thr Leu Tyr Thr	Met Phe Val Thr Trp Ser
	275	280 285
Ala Leu Ser Ser	Ile Pro Glu Gln Lys	Cys Asn Pro His Leu Pro
	290	295 300
Thr Gln Leu Gly	Asn Glu Thr Val Val	Ala Gly Pro Glu Gly Tyr
	305	310 315
Glu Thr Gln Trp	Trp Asp Ala Pro Ser	Ile Val Gly Leu Ile Ile
	320	325 330
Phe Leu Leu Cys	Thr Leu Phe Ile Ser	Leu Arg Ser Ser Asp His
	335	340 345
Arg Gln Val Asn	Ser Leu Met Gln Thr	Glu Glu Cys Pro Pro Met
	350	355 360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys Glu
	365	370 375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser Tyr
	380	385 390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val Met
	395	400 405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys Met
	410	415 420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser Trp
	425	430 435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu Leu
	440	445 450
Leu Arg Asn Arg	Asp Phe Ser	
	455	

<210> SEQ ID NO 13

<211> LENGTH: 1572

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 13

cgggccagcc tggggcggcc ggccaggaac caccggttaa ggtgtcttct	50
ctttagggat ggtgaggttg gaaaagact cctgtaacct tcctccagga	100
tgaaccacct gccagaagac atggagaacg ctctcaccgg gagccagagc	150
tcccatgctt ctctgcgcaa tatccattcc atcaacccca cacaactcat	200
ggccaggatt gagtcttatg aaggaaggga aaagaaaggc atatctgatg	250
tcaggaggac tttctgtttg tttgtcacct ttgacctctt attcgtaaca	300
ttactgtgga taatagagtt aaatgtgaat ggaggcattg agaacacatt	350
agagaaggag gtgatgcagt atgactacta ttcttcatat tttgatatat	400
ttcttctggc agtttttcga tttaaagtgt taatacttgc atatgctgtg	450
tgacagctgc gccattggtg ggcaatagcg ttgacaacgg cagtgaccag	500

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tgcccttttta ctagcaaaag tgatcctttc gaagcttttc tctcaagggg	550
cttttggtta tgtgctgccc atcatttcat tcctccttgc ctggattgag	600
acgtggttcc tggatttcaa agtggtacct caagaagcag aagaagaaaa	650
cagactcctg atagttcagg atgcttcaga gagggcagca cttatacctg	700
gtggtctttc tgatggtcag ttttattccc ctccgaatc cgaagcagga	750
tctgaagaag ctgaagaaaa acaggacagt gagaaccac ttttagaact	800
atgagtacta cttttgttaa atgtgaaaa ccctcacaga aagtcacga	850
ggcaaaaaga ggcaggcagt ggagtctccc tgctgacagt aaagttgaaa	900
tggtgacgtc cactgctggc tttattgaac agctaataaa gatttattta	950
ttgtaatacc tcacaaacgt tgtaccatat ccatgcacat ttagttgcct	1000
gcctgtggct ggtaaggtaa tgtcatgatt catcctctct tcagtgcagc	1050
tgagcctgat gtgttaacaa atagggaag aaagtcttgt gctgtattcc	1100
taatcaaaa acttaataata ttgaagtaac acttttttag taagcaagat	1150
acctttttat ttcaattcac agaattggaat ttttttgttt catgtctcag	1200
atttattttt tatttctttt ttaacactct acatttcctt tgttttttta	1250
ctcatgcaca tgtgctcttt gtacagtttt aaaaagtga ataaaactg	1300
acatgtcaat gtggctagtt ttatttttct tgttttgcat tatgtgtatg	1350
gcctgaagtg ttggacttgc aaaaggggaa gaaaggaatt gcgaatacat	1400
gtaaaatgtc accagacatt tgtattattt ttatcatgaa atcatgtttt	1450
tctctgattg ttctgaaatg ttctaaatac tcttattttg aatgcacaaa	1500
atgacttaaa ccattcatat catgtttcct ttgcgttcag ccaatttcaa	1550
ttaaaatgaa ctaaatataa aa	1572

<210> SEQ ID NO 14

<211> LENGTH: 234

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 14

Met Asn His Leu Pro Glu Asp Met Glu Asn Ala Leu Thr Gly Ser	
1 5 10 15	
Gln Ser Ser His Ala Ser Leu Arg Asn Ile His Ser Ile Asn Pro	
20 25 30	
Thr Gln Leu Met Ala Arg Ile Glu Ser Tyr Glu Gly Arg Glu Lys	
35 40 45	
Lys Gly Ile Ser Asp Val Arg Arg Thr Phe Cys Leu Phe Val Thr	
50 55 60	
Phe Asp Leu Leu Phe Val Thr Leu Leu Trp Ile Ile Glu Leu Asn	
65 70 75	
Val Asn Gly Gly Ile Glu Asn Thr Leu Glu Lys Glu Val Met Gln	
80 85 90	
Tyr Asp Tyr Tyr Ser Ser Tyr Phe Asp Ile Phe Leu Leu Ala Val	
95 100 105	
Phe Arg Phe Lys Val Leu Ile Leu Ala Tyr Ala Val Cys Arg Leu	
110 115 120	
Arg His Trp Trp Ala Ile Ala Leu Thr Thr Ala Val Thr Ser Ala	
125 130 135	

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Phe	Leu	Leu	Ala	Lys	Val	Ile	Leu	Ser	Lys	Leu	Phe	Ser	Gln	Gly
				140					145					150
Ala	Phe	Gly	Tyr	Val	Leu	Pro	Ile	Ile	Ser	Phe	Ile	Leu	Ala	Trp
				155					160					165
Ile	Glu	Thr	Trp	Phe	Leu	Asp	Phe	Lys	Val	Leu	Pro	Gln	Glu	Ala
				170					175					180
Glu	Glu	Glu	Asn	Arg	Leu	Leu	Ile	Val	Gln	Asp	Ala	Ser	Glu	Arg
				185					190					195
Ala	Ala	Leu	Ile	Pro	Gly	Gly	Leu	Ser	Asp	Gly	Gln	Phe	Tyr	Ser
				200					205					210
Pro	Pro	Glu	Ser	Glu	Ala	Gly	Ser	Glu	Glu	Ala	Glu	Glu	Lys	Gln
				215					220					225
Asp	Ser	Glu	Lys	Pro	Leu	Leu	Glu	Leu						
				230										

<210> SEQ ID NO 15

<211> LENGTH: 2768

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 15

actcgaacgc agttgcttcg ggaccacagga cccctcggg cccgaccgc	50
caggaaagac tgaggccgcg gcctgcccc cccggctccc tgcgccgcg	100
ccgctcccc ggacagaaga tgtgtccag ggtccctctg ctgctgccgc	150
tgctcctgct actggccctg gggcctggg tgcagggtg cccatccggc	200
tgccagtgc gccagccaca gacagtcttc tgactgccc gccaggggac	250
cacggtgccc cgagacgtgc caccgcacac ggtggggctg tacgtctttg	300
agaacggcat caccatgctc gacgcaggca gctttgccg cctgccgggc	350
ctgcagctcc tggacctgtc acagaaccag atcgccagcc tgcccagcgg	400
ggtcttccag ccaactcgcca acctagcaa cctggacctg acggccaaca	450
ggctgcatga aatcaccaat gagaccttc gtggcctgcg gcgcctcgag	500
cgcctctacc tgggcaagaa ccgcattccg cacatccagc ctggtgcctt	550
cgacacgtc gaccgcctcc tggagctcaa gctgcaggac aacgagctgc	600
gggcactgcc cccgctgcgc ctgccccgcc tgcgtctgct ggacctcagc	650
cacaacagcc tcctggccct ggagcccggc atcctggaca ctgccaacgt	700
ggaggcgctg cggtggctg gtctggggct gcagcagctg gacgaggggc	750
tcttcagccg ctgctgcaac ctccacgacc tggatgtgtc cgacaaccag	800
ctggagcgag tgccacctgt gatccgaggc ctccggggcc tgacgcgcct	850
gcggctggcc ggcaacaccc gcattgccca gctgcggccc gaggacctgg	900
ccggcctggc tgccctgcag gagctggatg tgagcaacct aagcctgcag	950
gccctgcctg gcgacctctc gggcctcttc cccgcctgc ggcgtctggc	1000
agctgcccg aaccccttca actgcgtgtg cccctgagc tggtttgcc	1050
cctgggtgcg cgagagccac gtcacactgg ccagccctga ggagacgcgc	1100
tgccacttcc cgccaagaa cgctggccgg ctgctcctgg agcttgacta	1150
cgccgacttt ggctgccag ccaccaccac cacagccaca gtgccacca	1200
cgaggcccg gtgctgggag cccacagcct tgtcttctag cttggctcct	1250

acctggctta gccccacag gccggccact gaggcccca gcccgccctc	1300
cactgcccc ccgactgtag ggctgtccc ccagccccag gactgcccac	1350
cgtccacctg cctcaatggg ggcacatgcc acctggggac acggcaccac	1400
ctggcggtgt tgtgccccga aggcttcacg ggctgtact gtgagagcca	1450
gatggggcag gggacacggc ccagccctac accagtccag ccgaggccac	1500
cacggtccct gaccctgggc atcgagccgg tgagccccac ctccctgcgc	1550
gtggggctgc agcgctacct ccaggggagc tccgtgcagc tcaggagcct	1600
ccgtctcacc tatcgcaacc tatcgggccc tgataagcgg ctggtgacgc	1650
tgcgactgcc tgccctcgct cctgagtaca cggtcaccca gctcgggccc	1700
aacgccactt actccgtctg tgtcatgctt ttggggcccg ggcggtgcc	1750
ggagggcgag gaggcctgcg gggaggccca tacaccccca gccgtccact	1800
ccaaccacgc cccagtcacc caggcccgcg agggcaacct gccgtcctc	1850
attgcgcccg ccttgccgcg ggtgctcctg gccgcgctgg ctgcggtggg	1900
ggcagcctac tgtgtgcggc gggggcgggc catggcagca gcggtcagg	1950
acaaagggca ggtggggcca ggggctgggc ccctggaact ggagggagtg	2000
aaggctccct tggagccagg cccgaaggca acagaggcgg gtggagaggc	2050
cctgcccagc gggctctgagt gtgaggtgcc actcatgggc ttcccagggc	2100
ctggcctcca gtcacccctc caccgaaagc cctacatcta agccagagag	2150
agacagggca gctggggcgc ggctctcagc cagtgcagtg gccagcccc	2200
tcctgctgcc acaccacgta agttctcagt cccaacctcg gggatgtgtg	2250
cagacagggc tgtgtgacca cagctgggcc ctgttccctc tggacctcgg	2300
tctcctcctc tgtgagatgc tgtggcccag ctgacgagcc ctaacgtccc	2350
cagaaccgag tgccctatgag gacagtgtcc gcctggccct ccgcaactgt	2400
cagtccctgg gcacggcggg ccctgccatg tgctggtaac gcatgcctgg	2450
gtcctgctgg gctctccca cccaggcgga ccctgggggc cagtgaagga	2500
agctcccgga aagagcagag ggagagcggg taggcggctg tgtgactcta	2550
gtcttgcccc caggaagcga aggaacaaaa gaaactggaa aggaagatgc	2600
tttaggaaca tgttttgctt ttttaaaata tatatattta taagagatcc	2650
tttcccatth attctgggaa gatgtttttc aaactcagag acaaggactt	2700
tggtttttgt aagacaaacg atgatatgaa ggccttttgt aagaaaaaat	2750
aaaagatgaa gtgtgaaa	2760

<400> SEQUENCE: 16

Ser Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr
35 40 45

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Val	Pro	Arg	Asp	Val	Pro	Pro	Asp	Thr	Val	Gly	Leu	Tyr	Val	Phe	50	55	60
Glu	Asn	Gly	Ile	Thr	Met	Leu	Asp	Ala	Gly	Ser	Phe	Ala	Gly	Leu	65	70	75
Pro	Gly	Leu	Gln	Leu	Leu	Asp	Leu	Ser	Gln	Asn	Gln	Ile	Ala	Ser	80	85	90
Leu	Pro	Ser	Gly	Val	Phe	Gln	Pro	Leu	Ala	Asn	Leu	Ser	Asn	Leu	95	100	105
Asp	Leu	Thr	Ala	Asn	Arg	Leu	His	Glu	Ile	Thr	Asn	Glu	Thr	Phe	110	115	120
Arg	Gly	Leu	Arg	Arg	Leu	Glu	Arg	Leu	Tyr	Leu	Gly	Lys	Asn	Arg	125	130	135
Ile	Arg	His	Ile	Gln	Pro	Gly	Ala	Phe	Asp	Thr	Leu	Asp	Arg	Leu	140	145	150
Leu	Glu	Leu	Lys	Leu	Gln	Asp	Asn	Glu	Leu	Arg	Ala	Leu	Pro	Pro	155	160	165
Leu	Arg	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Asp	Leu	Ser	His	Asn	Ser	170	175	180
Leu	Leu	Ala	Leu	Glu	Pro	Gly	Ile	Leu	Asp	Thr	Ala	Asn	Val	Glu	185	190	195
Ala	Leu	Arg	Leu	Ala	Gly	Leu	Gly	Leu	Gln	Gln	Leu	Asp	Glu	Gly	200	205	210
Leu	Phe	Ser	Arg	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp	215	220	225
Asn	Gln	Leu	Glu	Arg	Val	Pro	Pro	Val	Ile	Arg	Gly	Leu	Arg	Gly	230	235	240
Leu	Thr	Arg	Leu	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Leu	245	250	255
Arg	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Ala	Ala	Leu	Gln	Glu	Leu	Asp	260	265	270
Val	Ser	Asn	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Gly	Asp	Leu	Ser	Gly	275	280	285
Leu	Phe	Pro	Arg	Leu	Arg	Leu	Leu	Ala	Ala	Ala	Arg	Asn	Pro	Phe	290	295	300
Asn	Cys	Val	Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu	305	310	315
Ser	His	Val	Thr	Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe	320	325	330
Pro	Pro	Lys	Asn	Ala	Gly	Arg	Leu	Leu	Leu	Glu	Leu	Asp	Tyr	Ala	335	340	345
Asp	Phe	Gly	Cys	Pro	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr	350	355	360
Thr	Arg	Pro	Val	Val	Arg	Glu	Pro	Thr	Ala	Leu	Ser	Ser	Ser	Leu	365	370	375
Ala	Pro	Thr	Trp	Leu	Ser	Pro	Thr	Ala	Pro	Ala	Thr	Glu	Ala	Pro	380	385	390
Ser	Pro	Pro	Ser	Thr	Ala	Pro	Pro	Thr	Val	Gly	Pro	Val	Pro	Gln	395	400	405
Pro	Gln	Asp	Cys	Pro	Pro	Ser	Thr	Cys	Leu	Asn	Gly	Gly	Thr	Cys	410	415	420
His	Leu	Gly	Thr	Arg	His	His	Leu	Ala	Cys	Leu	Cys	Pro	Glu	Gly	425	430	435
Phe	Thr	Gly	Leu	Tyr	Cys	Glu	Ser	Gln	Met	Gly	Gln	Gly	Thr	Arg			

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440	445	450
Pro Ser Pro Thr 455	Pro Val Thr Pro Arg 460	Pro Pro Arg Ser Leu Thr 465
Leu Gly Ile Glu 470	Pro Val Ser Pro Thr 475	Ser Leu Arg Val Gly Leu 480
Gln Arg Tyr Leu 485	Gln Gly Ser Ser Val 490	Gln Leu Arg Ser Leu Arg 495
Leu Thr Tyr Arg 500	Asn Leu Ser Gly Pro 505	Asp Lys Arg Leu Val Thr 510
Leu Arg Leu Pro 515	Ala Ser Leu Ala Glu 520	Tyr Thr Val Thr Gln Leu 525
Arg Pro Asn Ala 530	Thr Tyr Ser Val Cys 535	Val Met Pro Leu Gly Pro 540
Gly Arg Val Pro 545	Glu Gly Glu Glu Ala 550	Cys Gly Glu Ala His Thr 555
Pro Pro Ala Val 560	His Ser Asn His Ala 565	Pro Val Thr Gln Ala Arg 570
Glu Gly Asn Leu 575	Pro Leu Leu Ile Ala 580	Pro Ala Leu Ala Ala Val 585
Leu Leu Ala Ala 590	Leu Ala Ala Val Gly 595	Ala Ala Tyr Cys Val Arg 600
Arg Gly Arg Ala 605	Met Ala Ala Ala Ala 610	Gln Asp Lys Gly Gln Val 615
Gly Pro Gly Ala 620	Gly Pro Leu Glu Leu 625	Glu Gly Val Lys Val Pro 630
Leu Glu Pro Gly 635	Pro Lys Ala Thr Glu 640	Gly Gly Gly Glu Ala Leu 645
Pro Ser Gly Ser 650	Glu Cys Glu Val Pro 655	Leu Met Gly Phe Pro Gly 660
Pro Gly Leu Gln 665	Ser Pro Leu His Ala 670	Lys Pro Tyr Ile

<210> SEQ ID NO 17

<211> LENGTH: 1672

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 17

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gcagcggcga ggcggcggtg gtggctgagt ccgtggtggc agaggcgaag      50
gcgacagctc atgcgggtcc ggatagggct gacgctgctg ctgtgtgcgg      100
tgctgctgag cttggcctcg gcgtcctcgg atgaagaagg cagccaggat      150
gaatccttag attccaagac tactttgaca tcagatgagt cagtaaagga      200
ccatactact gcaggcagag tagttgctgg tcaaatatit cttgattcag      250
aagaatctga attagaatcc tctattcaag aagaggaaga cagcctcaag      300
agccaagagg gggaaagtgt cacagaagat atcagctttc tagagtctcc      350
aaatccagaa aacaaggact atgaagagcc aaagaaagta cggaaccag      400
ctttgaccgc cattgaaggc acagcacatg gggagccctg ccacttcctt      450
tttcttttcc tagataagga gtatgatgaa tgtacatcag atgggaggga      500
agatggcaga ctgtggtgtg ctacaaccta tgactacaaa gcagatgaaa      550
agtggggcct ttgtgaaact gaagaagagg ctgctaagag acggcagatg      600

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caggaagcag aaatgatgta tcaaactgga atgaaaatcc ttaatggaag	650
caataagaaa agccaaaaaa gagaagcata tcggtatctc caaaaggcag	700
caagcatgaa ccataccaaa gccctggaga gagtgcata tgctctttta	750
tttggtgatt acttgccaca gaatatccag gcagcgagag agatgtttga	800
gaagctgact gaggaaggct ctccaaggag acagactgct cttggctttc	850
tgatgcctc tggacttggt gttaattcaa gtcaggcaaa ggctcttgta	900
tattatacat ttggagctct tgggggcaat ctaatagccc acatggtttt	950
ggtaagtaga ctttagtgga aggctaataa tattaacatc agaagaattt	1000
gtggtttata gcggccacaa ctttttcagc tttcatgac cagatttgct	1050
tgtattaaga ccaaattatc agttgaactt ccttcaaatt cttgttaatg	1100
gatataacac atggaatcta catgtaaatg aaagttggtg gagtccacaa	1150
tttttcttta aaatgattag ttggctgat tgcccctaaa aagagagatc	1200
tgataaatgg ctctttttta attttctctg agttggaatt gtcagaatca	1250
ttttttacat tagattatca taattttaaa aatttttctt tagtttttca	1300
aaattttgta aatggtggct atagaaaaac aacatgaaat attatacaat	1350
attttgcaac aatgccctaa gaattgttaa aattcatgga gttatttggtg	1400
cagaatgact ccagagagct ctactttctg ttttttactt ttcatgattg	1450
gctgtcttcc catttattct ggtcatttat tgctagtac actgtgcctg	1500
cttcagtag tctcattttc cctattttgc taatttgta ctttttcttt	1550
gctaatttgg aagattaact catttttaat aaaattatgt ctaagattaa	1600
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1650
aaaaaaaaa aaaaaaaaaa aa	1672

<210> SEQ ID NO 18

<211> LENGTH: 301

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 18

Met Arg Val Arg	Ile Gly Leu Thr	Leu Leu Leu Cys	Ala Val Leu
1	5	10	15
Leu Ser Leu Ala	Ser Ala Ser Ser	Asp Glu Gly Ser	Gln Asp
20	25	30	
Glu Ser Leu Asp	Ser Lys Thr Thr	Leu Thr Ser	Asp Glu Ser Val
35	40	45	
Lys Asp His Thr	Thr Ala Gly Arg	Val Val Ala Gly	Gln Ile Phe
50	55	60	
Leu Asp Ser Glu	Glu Ser Glu Leu	Glu Ser Ser	Ile Gln Glu Glu
65	70	75	
Glu Asp Ser Leu	Lys Ser Gln Glu	Gly Glu Ser	Val Thr Glu Asp
80	85	90	
Ile Ser Phe Leu	Glu Ser Pro Asn	Pro Glu Asn	Lys Asp Tyr Glu
95	100	105	
Glu Pro Lys Lys	Val Arg Lys Pro	Ala Leu Thr	Ala Ile Glu Gly
110	115	120	
Thr Ala His Gly	Glu Pro Cys His	Phe Pro Phe	Leu Phe Leu Asp
125	130	135	

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Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp	Gly	Arg	Glu	Asp	Gly	Arg
				140					145					150
Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys	Ala	Asp	Glu	Lys	Trp
				155					160					165
Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met
				170					175					180
Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys	Ile	Leu	Asn
				185					190					195
Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg	Tyr	Leu
				200					205					210
Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg	Val
				215					220					225
Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln
				230					235					240
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro
				245					250					255
Lys	Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly
				260					265					270
Val	Asn	Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly
				275					280					285
Ala	Leu	Gly	Gly	Asn	Leu	Ile	Ala	His	Met	Val	Leu	Val	Ser	Arg
				290					295					300

Leu

<210> SEQ ID NO 19
 <211> LENGTH: 1508
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 19

aattcagatt ttaagcccat tctgcagtgg aatttcata ga actagcaaga	50
ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac	100
agggggaaaa atgctctttt ggggtgctagg cctcctaata ctctgtgggt	150
ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag	200
tacattttta tcaactggatg tgactcgggc ttgggaaact tggcagccag	250
aaacttttgat aaaaagggat ttcattgtaat cgctgcctgt ctgactgaat	300
caggatcaac agcttttaaag gcagaaacct cagagagact tcgtactgtg	350
cttctggatg tgaccgaccc agagaatgtc aagaggactg ccagtggggt	400
gaagaaccaa gttggggaga aaggtctctg gggctctgac aataatgctg	450
gtgttcccgg cgtgctggct cccactgact ggctgacact agaggactac	500
agagaaccta ttgaagtga cctgtttgga ctcatcagt tgacactaaa	550
tatgcttcct ttggtaaga aagctcaagg gagagttatt aatgtctcca	600
gtgttgagg tcgccttgca atcgttgagg ggggtatata tccatccaaa	650
tatgcagtgg aaggtttcaa tgacagctta agacgggaca tgaagcttt	700
tggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttg	750
cagatccagt aaagtaatt gaaaaaaac tcgccatttg ggagcagctg	800
tctccagaca tcaacaaca atatggagaa ggttacattg aaaaagtct	850
agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg	900

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tggtagagtg catggaccac gctctaacaa gtctcttccc taagactcat	950
tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat	1000
gccagcagct ttgcaagact ttttattggt gaaacagaaa gcagagctgg	1050
ctaattcccaa ggcagtggtga ctcagctaac cacaaatgtc tcctccaggc	1100
tatgaaattg gccgatttca agaacacatc tccttttcaa ccccatctct	1150
tatctgctcc aacctggact catttagatc gtgcttattt ggattgcaaa	1200
agggagtccc accatcgctg gtggtatccc agggtcctcg ctcaagtttt	1250
ctttgaaaag gagggctgga atggtacatc acataggcaa gtcctgcctt	1300
gtatttaggc ttgctctgct tgggtgatg taagggaat tgaagactt	1350
gcccattcaa aatgatcttt accgtggcct gcccctatgct tatggtcccc	1400
agcatttaca gtaacttggt aatgttaagt atcatctctt atctaaatat	1450
taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1500
aaaaaaaa	1508

<210> SEQ ID NO 20

<211> LENGTH: 319

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 20

Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu	
1 5 10 15	
Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys	
20 25 30	
Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala	
35 40 45	
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys	
50 55 60	
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu	
65 70 75	
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val	
80 85 90	
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly	
95 100 105	
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala	
110 115 120	
Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu	
125 130 135	
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro	
140 145 150	
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val	
155 160 165	
Gly Gly Arg Leu Ala Ile Val Gly Gly Gly Tyr Thr Pro Ser Lys	
170 175 180	
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys	
185 190 195	
Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys	
200 205 210	
Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala	
215 220 225	

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Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260						265				270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275						280				285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290						295				300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305						310				315
Pro	Lys	Ala	Val											

<210> SEQ ID NO 21
 <211> LENGTH: 1849
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 21

ctgagcgccg gtagcatgg agggggagag tacgtcggcg gtgctctcgg	50
gctttgtgct cggcgcactc gctttccagc acctcaacac ggactcggac	100
acggaagggt ttcttcttgg ggaagtaaaa ggtgaagcca agaacagcat	150
tactgattcc caaatggatg atgttgaagt tgtttataca attgacattc	200
agaaatatat tccatgctat cagcttttta gcttttataa ttcttcaggc	250
gaagtaaatg agcaagcact gaagaaaata ttatcaaatg tcaaaaagaa	300
tgtggtagggt tggtaacaaat tccgtcgtca ttcagatcag atcatgacgt	350
ttagagagag gctgcttcac aaaaacttgc aggagcattt ttcaaaccac	400
gaccttggtt ttctgctatt aacaccaagt ataataacag aaagctgctc	450
tactcatcga ctggaacatt ccttatataa acctcaaaaa ggactttttc	500
acagggtagc tttagtgggt gccaatctgg gcattgtctga acaactgggt	550
tataaaactg tatcagggtc ctgtatgtcc actggtttta gccgagcagt	600
acaaacacac agctctaaat tttttgaaga agatggatcc ttaaaggagg	650
tacataagat aaatgaaatg tatgcttcac tacaagagga attaaagagt	700
atatgcaaaa aagtgggaaga cagtgaacaa gcagtagata aactagtaaa	750
ggatgtaaac agattaaaac gagaaattga gaaaaggaga ggagcacaga	800
ttcaggcagc aagagagaag aacatccaaa aagaccctca ggagaacatt	850
tttctttgtc aggcattacg gacctttttt ccaaattctg aatttcttca	900
ttcatgtgtt atgtctttta aaaatagaca tgtttctaaa agtagctgta	950
actacaacca ccatctcgat gtagtagaca atctgacctt aatggtagaa	1000
cacactgaca ttctgaagc tagtccagct agtacaccac aaatcattaa	1050
gcataaagcc ttagacttag atgacagatg gcaattcaag agatctcgggt	1100
tgttagatac acaagacaaa cgatctaaag caaatactgg tagtagtaac	1150
caagataaag catccaaaat gagcagccca gaaacagatg aagaaattga	1200
aaagatgaag ggttttggtg aatattcacg gtctcctaca ttttgatcct	1250
tttaacctta caaggagatt tttttatttg gctgatgggt aaagccaaac	1300

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atttctattg tttttactat gttgagctac ttgcagtaag ttcatttggt      1350
tttactatgt tcacctgttt gcagtaatac acagataact cttagtgcac      1400
ttacttcaca aagtactttt tcaaacatca gatgctttta tttccaaacc      1450
tttttttcac ctttcactaa gttgttgagg ggaaggctta cacagacaca      1500
ttcttttagaa ttggaaaagt gagaccaggc acagtggctc acacctgtaa      1550
tcccagcact tagggaagac aagtcaggag gattgattga agctaggagt      1600
tagagaccag cctgggcaac gtattgagac catgtctatt aaaaaataaa      1650
atggaaaagc aagaatagcc ttattttcaa aatatggaaa gaaatttata      1700
tgaaaattta tctgagtcac taaaattctc cttaagtgat acttttttag      1750
aagtacatta tggctagagt tgccagataa aatgctggat atcatgcaat      1800
aaatttgcaa aacatcatct aaaattttaa aaaaaaaaaa aaaaaaaaaa      1849

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<210> SEQ ID NO 22

<211> LENGTH: 409

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 22

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Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu
 1             5             10            15
Gly Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu
 20            25            30
Gly Phe Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile
 35            40            45
Thr Asp Ser Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp
 50            55            60
Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn
 65            70            75
Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser
 80            85            90
Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg His
 95           100           105
Ser Asp Gln Ile Met Thr Phe Arg Glu Arg Leu Leu His Lys Asn
110           115           120
Leu Gln Glu His Phe Ser Asn Gln Asp Leu Val Phe Leu Leu Leu
125           130           135
Thr Pro Ser Ile Ile Thr Glu Ser Cys Ser Thr His Arg Leu Glu
140           145           150
His Ser Leu Tyr Lys Pro Gln Lys Gly Leu Phe His Arg Val Pro
155           160           165
Leu Val Val Ala Asn Leu Gly Met Ser Glu Gln Leu Gly Tyr Lys
170           175           180
Thr Val Ser Gly Ser Cys Met Ser Thr Gly Phe Ser Arg Ala Val
185           190           195
Gln Thr His Ser Ser Lys Phe Phe Glu Glu Asp Gly Ser Leu Lys
200           205           210
Glu Val His Lys Ile Asn Glu Met Tyr Ala Ser Leu Gln Glu Glu
215           220           225
Leu Lys Ser Ile Cys Lys Lys Val Glu Asp Ser Glu Gln Ala Val
230           235           240

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aattctgagc tatttaaaga tctcttcgta gagggtgaaac gttactacgt	950
ggtagggaaat gtgaacctgg aagaaatgct aaatgacttc tgggctcgcc	1000
tcctggagcg gatgttcgcc ctggtgaact cccagtacca ctttacagat	1050
gagtatctgg aatgtgtgag caagtatacg gagcagctga agcccttcgg	1100
agatgtccct cgcaaattga agctccaggt tactcgtgct tttgtagcag	1150
cccgtacttt cgctcaaggc ttagcgggtg cgggagatgt cgtgagcaag	1200
gtctccgtgg taaacccac agcccagtgt acccatgccc tgttgaagat	1250
gactactgct tcccactgcc ggggtctcgt gactgtgaag ccatgttaca	1300
actactgctc aaacatcatg agaggctgtt tggccaacca aggggacttc	1350
gattttgaat ggaacaattt catagatgct atgctgatgg tggcagagag	1400
gctagagggc cctttcaaca ttgaatcggc catggatccc atcgaatgta	1450
agatttctga tgctattatg aacatgcagg ataatagtgt tcaagtgtct	1500
cagaagggtt tccagggatg tggacccccc aagccctcc cagctggacg	1550
aatttctcgt tccatctctg aaagtgcctt cagtgcctcg ttcagaccac	1600
atcacccga ggaacgcca accacagcag ctggcactag tttggaccga	1650
ctggttactg atgtcaagga gaaactgaaa caggccaaga aattctggtc	1700
ctccctccg agcaacgttt gcaacgatga gaggatggct gcaggaaacg	1750
gcaatgagga tgactgttgg aatgggaaag gcaaaagcag gtacctgttt	1800
gcagtgcag gaaatggatt agccaaccag ggcaacaacc cagaggtcca	1850
ggttgacacc agcaaaccag acatactgat ccttcgtcaa atcatggctc	1900
ttcgaatgat gaccagcaag atgaagaatg catacaatgg gaacgacgtg	1950
gacttctttg atatcagtga tgaaagtagt ggagaaggaa gtggaagtgg	2000
ctgtgagtat cagcagtgcc cttcagagtt tgactacaat gccactgacc	2050
atgctgggaa gagtgcgaat gagaaagccg acagtgcgtg tgtccgtcct	2100
ggggcacagg cctacctcct cactgtcttc tgcactctgt tcctggttat	2150
gcagagagag tggagataat tctcaaacct tgagaaaaag tgttcacaa	2200
aaagttaaaa ggcaccagtt atcacttttc taccatccta gtgactttgc	2250
tttttaaatg aatggacaac aatgtacagt ttttactatg tggccactgg	2300
tttaagaagt gctgactttg ttttctcatt cagttttggg aggaaaagg	2350
actgtgcatt gagttggttc ctgctccccc aaaccatgtt aaacgtggct	2400
aacagtgtag gtacagaact atagttagtt gtgcatttgt gattttatca	2450
ctctattatt tgtttgtatg tttttttctc atttcgtttg tgggtttttt	2500
tttccaactg tgatctcgcc ttgtttctta caagcaaac agggctccct	2550
cttggcagct aacatgtacg tatttctgaa atattaaata gctgtacaga	2600
agcaggtttt atttatcatg ttatcttatt aaaagaaaa gcccaaaaag	2650
c	2651

<210> SEQ ID NO 24

<211> LENGTH: 556

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 24

-continued

Met	Ala	Arg	Phe	Gly	Leu	Pro	Ala	Leu	Leu	Cys	Thr	Leu	Ala	Val	1	5	10	15
Leu	Ser	Ala	Ala	Leu	Leu	Ala	Ala	Glu	Leu	Lys	Ser	Lys	Ser	Cys	20	25	30	
Ser	Glu	Val	Arg	Arg	Leu	Tyr	Val	Ser	Lys	Gly	Phe	Asn	Lys	Asn	35	40	45	
Asp	Ala	Pro	Leu	His	Glu	Ile	Asn	Gly	Asp	His	Leu	Lys	Ile	Cys	50	55	60	
Pro	Gln	Gly	Ser	Thr	Cys	Cys	Ser	Gln	Glu	Met	Glu	Glu	Lys	Tyr	65	70	75	
Ser	Leu	Gln	Ser	Lys	Asp	Asp	Phe	Lys	Ser	Val	Val	Ser	Glu	Gln	80	85	90	
Cys	Asn	His	Leu	Gln	Ala	Val	Phe	Ala	Ser	Arg	Tyr	Lys	Lys	Phe	95	100	105	
Asp	Glu	Phe	Phe	Lys	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120	
Asn	Asp	Met	Phe	Val	Lys	Thr	Tyr	Gly	His	Leu	Tyr	Met	Gln	Asn	125	130	135	
Ser	Glu	Leu	Phe	Lys	Asp	Leu	Phe	Val	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150	
Val	Val	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165	
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Arg	Leu	Val	Asn	Ser	Gln	Tyr	170	175	180	
His	Phe	Thr	Asp	Glu	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Glu	185	190	195	
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Leu	Gln	200	205	210	
Val	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Thr	Phe	Ala	Gln	Gly	Leu	215	220	225	
Ala	Val	Ala	Gly	Asp	Val	Val	Ser	Lys	Val	Ser	Val	Val	Asn	Pro	230	235	240	
Thr	Ala	Gln	Cys	Thr	His	Ala	Leu	Leu	Lys	Met	Ile	Tyr	Cys	Ser	245	250	255	
His	Cys	Arg	Gly	Leu	Val	Thr	Val	Lys	Pro	Cys	Tyr	Asn	Tyr	Cys	260	265	270	
Ser	Asn	Ile	Met	Arg	Gly	Cys	Leu	Ala	Asn	Gln	Gly	Asp	Leu	Asp	275	280	285	
Phe	Glu	Trp	Asn	Asn	Phe	Ile	Asp	Ala	Met	Leu	Met	Val	Ala	Glu	290	295	300	
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315	
Asp	Val	Lys	Ile	Ser	Asp	Ala	Ile	Met	Asn	Met	Gln	Asp	Asn	Ser	320	325	330	
Val	Gln	Val	Ser	Gln	Lys	Val	Phe	Gln	Gly	Cys	Gly	Pro	Pro	Lys	335	340	345	
Pro	Leu	Pro	Ala	Gly	Arg	Ile	Ser	Arg	Ser	Ile	Ser	Glu	Ser	Ala	350	355	360	
Phe	Ser	Ala	Arg	Phe	Arg	Pro	His	His	Pro	Glu	Glu	Arg	Pro	Thr	365	370	375	
Thr	Ala	Ala	Gly	Thr	Ser	Leu	Asp	Arg	Leu	Val	Thr	Asp	Val	Lys	380	385	390	

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Glu	Lys	Leu	Lys	Gln	Ala	Lys	Lys	Phe	Trp	Ser	Ser	Leu	Pro	Ser
			395						400				405	
Asn	Val	Cys	Asn	Asp	Glu	Arg	Met	Ala	Ala	Gly	Asn	Gly	Asn	Glu
			410						415				420	
Asp	Asp	Cys	Trp	Asn	Gly	Lys	Gly	Lys	Ser	Arg	Tyr	Leu	Phe	Ala
			425						430				435	
Val	Thr	Gly	Asn	Gly	Leu	Ala	Asn	Gln	Gly	Asn	Asn	Pro	Glu	Val
			440						445				450	
Gln	Val	Asp	Thr	Ser	Lys	Pro	Asp	Ile	Leu	Ile	Leu	Arg	Gln	Ile
			455						460				465	
Met	Ala	Leu	Arg	Val	Met	Thr	Ser	Lys	Met	Lys	Asn	Ala	Tyr	Asn
			470						475				480	
Gly	Asn	Asp	Val	Asp	Phe	Phe	Asp	Ile	Ser	Asp	Glu	Ser	Ser	Gly
			485						490				495	
Glu	Gly	Ser	Gly	Ser	Gly	Cys	Glu	Tyr	Gln	Gln	Cys	Pro	Ser	Glu
			500						505				510	
Phe	Asp	Tyr	Asn	Ala	Thr	Asp	His	Ala	Gly	Lys	Ser	Ala	Asn	Glu
			515						520				525	
Lys	Ala	Asp	Ser	Ala	Gly	Val	Arg	Pro	Gly	Ala	Gln	Ala	Tyr	Leu
			530						535				540	
Leu	Thr	Val	Phe	Cys	Ile	Leu	Phe	Leu	Val	Met	Gln	Arg	Glu	Trp
			545						550				555	

Arg

<210> SEQ ID NO 25

<211> LENGTH: 870

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 25

ctcgccctca aatgggaacg ctggcctggg actaaagcat agaccaccag	50
gctgagtatc ctgacctgag tcatccccag ggatcaggag cctccagcag	100
ggaaccttcc attatatctt tcaagcaact tacagctgca cgcacagtgt	150
cgatgaaagt tctaattctt tccctcctcc tgttgctgcc actaatgctg	200
atgtccatgg tctctagcag cctgaatcca ggggtcgcca gaggccacag	250
ggaccgaggc caggcttcta ggagatggct ccaggaaggc ggccaagaat	300
gtgagtgcaa agattgggtc ctgagagccc cgagaagaaa attcatgaca	350
gtgtctgggc tgccaaagaa gcagtgcctc tgtgatcatt tcaagggcaa	400
tgtgaagaaa acaagacacc aaaggcacca cagaaagcca aacaagcatt	450
ccagagcctg ccagcaattt ctcaacaat gtcagctaag aagctttgct	500
ctgcctttgt aggagctctg agcgccact cttccaatta aacattctca	550
gccaagaaga cagtgcagc acctaccaga cactcttctt cttccacctc	600
actctccacc tgtaccacc cctaaatcat tccagtgtc tcaaaaagca	650
tggttttcaa gatcattttg ttgtgtgtc tctctagtgt cttcttctct	700
cgtcagtcct agcctgtgcc ctccccttac ccaggcttag gcttaattac	750
ctgaaagatt ccaggaaact gtagcttcct agctagtgtc atttaacctt	800
aaatgcaatc aggaagtag caaacagaag tcaataaata tttttaaatg	850
tcaaaaaaaaa aaaaaaaaaa	870

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<210> SEQ ID NO 26
 <211> LENGTH: 119
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 26

Met	Lys	Val	Leu	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Pro	Leu	Met		
1				5					10				15		
Leu	Met	Ser	Met	Val	Ser	Ser	Ser	Leu	Asn	Pro	Gly	Val	Ala	Arg	
				20					25					30	
Gly	His	Arg	Asp	Arg	Gly	Gln	Ala	Ser	Arg	Arg	Trp	Leu	Gln	Glu	
				35					40					45	
Gly	Gly	Gln	Glu	Cys	Glu	Cys	Lys	Asp	Trp	Phe	Leu	Arg	Ala	Pro	
				50					55					60	
Arg	Arg	Lys	Phe	Met	Thr	Val	Ser	Gly	Leu	Pro	Lys	Lys	Gln	Cys	
				65					70					75	
Pro	Cys	Asp	His	Phe	Lys	Gly	Asn	Val	Lys	Lys	Thr	Arg	His	Gln	
				80					85					90	
Arg	His	His	Arg	Lys	Pro	Asn	Lys	His	Ser	Arg	Ala	Cys	Gln	Gln	
				95					100					105	
Phe	Leu	Lys	Gln	Cys	Gln	Leu	Arg	Ser	Phe	Ala	Leu	Pro	Leu		
				110					115						

<210> SEQ ID NO 27
 <211> LENGTH: 1371
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 27

ggagcgcagc gcctgcagag gctgagcagg gaaaaagcca gtgccccagc	50
ggaagcacag ctcagagctg gtctgccatg gacatcctgg tcccactcct	100
gcagctgctg gtgctgcttc ttaccctgcc cctgcacctc atggctctgc	150
tgggtgctg gcagcccctg tgcaaaagct acttccccta cctgatggcc	200
gtgtgtgact ccaagagcaa ccgcaagatg gagagcaaga aacgggagct	250
cttcagccag ataaaggggc ttacaggagc ctccgggaaa gtggccctac	300
tggagctggg ctgcggaacc ggagccaact ttcagttcta cccaccgggc	350
tgcaggggtca cctgcctaga cccaaatccc cactttgaga agttcctgac	400
aaagagcatg gctgagaaca ggcacctcca atatgagcgg tttgtggtg	450
ctcctggaga ggacatgaga cagctggctg atggctccat ggatgtggtg	500
gtctgcactc tgggtgctgt ctctgtgcag agcccaagga aggtcctgca	550
ggaggtccgg agagtactga gaccgggagg tgtgctcttt ttctgggagc	600
atgtggcaga accatatgga agctgggcct tcatgtggca gcaagttttc	650
gagcccacct ggaaacacat tggggatggc tgctgcctca ccagagagac	700
ctggaaggat cttgagaacg ccagttctc cgaaatccaa atggaacgac	750
agccccctcc cttgaagtgg ctacctgttg ggccccacat catgggaaag	800
gctgtcaaac aatctttccc aagctccaag gcaactcatt gtccttccc	850
cagcctccaa ttagaacaag ccaccacca gcctatctat cttccactga	900
gaggaccta gcagaatgag agaagacatt catgtaccac ctactagtcc	950
ctctctcccc aacctctgcc agggcaatct ctaacttcaa tcccgcttc	1000

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gacagtga aaagctctact tctacgtga cccagggagg aaacactagg      1050
accctgttgt atcctcaact gcaagtttct ggactagtct cccaacgttt      1100
gcctcccaat gttgtccctt tccttcgttc ccatggtaaa gtcctctctg      1150
ctttcctcct gaggctacac ccatgcgtct ctaggaactg gtcacaaaag      1200
tcatggtgcc tgcacccctg ccaagccccc ctgaccctct cccccacta      1250
ccaccttctt cctgagctgg gggcaccagg gagaatcaga gatgctgggg      1300
atgccagagc aagactcaaa gaggcagagg ttttgttctc aaatattttt      1350
taataaatag acgaaaccac g                                     1371

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<210> SEQ ID NO 28
<211> LENGTH: 277
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 28

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Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu
 1           5           10          15
Thr Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro
 20          25          30
Leu Cys Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro
 35          40          45
Lys Ser Asn Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser
 50          55          60
Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu
 65          70          75
Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro
 80          85          90
Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His Phe Glu Lys
 95          100         105
Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln Tyr Glu
 110         115         120
Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala Asp
 125         130         135
Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val
 140         145         150
Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg
 155         160         165
Pro Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr
 170         175         180
Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp
 185         190         195
Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys
 200         205         210
Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln
 215         220         225
Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
 230         235         240
Lys Ala Val Lys Gln Ser Phe Pro Ser Ser Lys Ala Leu Ile Cys
 245         250         255
Ser Phe Pro Ser Leu Gln Leu Glu Gln Ala Thr His Gln Pro Ile
 260         265         270

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Tyr Leu Pro Leu Arg Gly Thr
275

<210> SEQ ID NO 29
<211> LENGTH: 494
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 29

caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct	50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg	100
gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg	150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcacggcc	200
tgccatgacc tgcagccaag cccagcccg tggggaagg gagaaagtgg	250
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg	300
ggctaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta	350
atttatatac agatattaag gccctgttca ttaagaaatt gttcccttcc	400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa	450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa	494

<210> SEQ ID NO 30
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 30

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly	1 5 10 15
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser	20 25 30
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser	35 40 45
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln	50 55 60
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly	65 70

<210> SEQ ID NO 31
<211> LENGTH: 1660
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 31

gtttgaattc cttcaactat acccacagtc caaaagcaga ctactgtgt	50
cccaggctac cagttcctcc aagcaagtca tttcccttat ttaaccgatg	100
tgccctcaa acacctgagt gctactccct atttgcattc gttttgataa	150
atgatgttga caccctccac cgaattctaa gtggaatcat gtcgggaaga	200
gatacaatcc ttggcctgtg tatcctcgca ttacgcttgt ctttggccat	250
gatgtttacc ttcagattca tcaccaccct tctgggttcac attttcattt	300
cattgggttat ttggggattg ttgtttgtct gcggtgtttt atggtggctg	350
tattatgact ataccaacga cctcagcata gaattggaca cagaaaggga	400
aaatatgaag tgcgtgctgg ggtttgctat cgtatccaca ggcatcacgg	450

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cagtgtctgct cgtcttgatt tttgttctca gaaagagaat aaaattgaca	500
gttgagcttt tccaaatcac aaataaagcc atcagcagtg ctcccttcct	550
gctgttccag ccaactgtgga catttgccat cctcattttc ttctgggtcc	600
tctgggtggc tgtgtgtgtg agcctgggaa ctgcaggagc tgcccagggt	650
atggaaggcg gccaaagtga atataagccc ctttcgggca ttcggtacat	700
gtggtcgtac catttaattg gcctcatctg gactagttaa ttcacccctg	750
cgtgccagca aatgactata gctggggcag tggttacttg ttatttcaac	800
agaagtaaaa atgatcctcc tgatcatccc atcctttcgt ctctctccat	850
tctcttcttc taccatcaag gaaccgttgt gaaagggtca tttttaatct	900
ctgtgtgtgag gattccgaga atcattgtca tgtacatgca aaacgcactg	950
aaagaacagc agcatggtgc attgtccagg tacctgttcc gatgctgcta	1000
ctgctgtttc tgggtgtcttg acaataacct gctccatctc aaccagaatg	1050
catatactac aactgctatt aatgggacag atttctgtac atcagcaaaa	1100
gatgcattca aaatctgtc caagaactca agtcacttta catctattaa	1150
ctgctttgga gacttcataa tttttctagg aaagggtgta gtggtgtgtt	1200
tcactgtttt tggaggactc atgggtttta actacaatcg ggcattccag	1250
gtgtgggcag tccctctgtt attggtagct ttttttgcct acttagtagc	1300
ccatagtttt ttatctgtgt ttgaaactgt gctggatgca cttttcctgt	1350
gttttgctgt tgatctggaa acaaatgatg gatcgtcaga aaagccctac	1400
tttatggatc aagaatttct gagtttcgta aaaaggagca acaaatataa	1450
caatgcaagg gcacagcagg acaagcactc attaaggaat gaggagggaa	1500
cagaactcca ggccattgtg agatagatac ccatttaggt atctgtacct	1550
ggaaaacatt tccttctaag agccatttac agaatagaag atgagaccac	1600
tagagaaaag ttagtgaatt tttttttaaa agacctaata aaccctattc	1650
ttcctcaaaa	1660

<210> SEQ ID NO 32

<211> LENGTH: 445

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 32

Met	Ser	Gly	Arg	Asp	Thr	Ile	Leu	Gly	Leu	Cys	Ile	Leu	Ala	Leu
1				5					10					15
Ala	Leu	Ser	Leu	Ala	Met	Met	Phe	Thr	Phe	Arg	Phe	Ile	Thr	Thr
				20					25					30
Leu	Leu	Val	His	Ile	Phe	Ile	Ser	Leu	Val	Ile	Leu	Gly	Leu	Leu
				35					40					45
Phe	Val	Cys	Gly	Val	Leu	Trp	Trp	Leu	Tyr	Tyr	Asp	Tyr	Thr	Asn
				50					55					60
Asp	Leu	Ser	Ile	Glu	Leu	Asp	Thr	Glu	Arg	Glu	Asn	Met	Lys	Cys
				65					70					75
Val	Leu	Gly	Phe	Ala	Ile	Val	Ser	Thr	Gly	Ile	Thr	Ala	Val	Leu
				80					85					90
Leu	Val	Leu	Ile	Phe	Val	Leu	Arg	Lys	Arg	Ile	Lys	Leu	Thr	Val
				95					100					105

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Glu Leu Phe Gln Ile Thr Asn Lys Ala	Ile Ser Ser Ala Pro Phe
110	115 120
Leu Leu Phe Gln Pro Leu Trp Thr Phe	Ala Ile Leu Ile Phe Phe
125	130 135
Trp Val Leu Trp Val Ala Val Leu Leu	Ser Leu Gly Thr Ala Gly
140	145 150
Ala Ala Gln Val Met Glu Gly Gly Gln	Val Glu Tyr Lys Pro Leu
155	160 165
Ser Gly Ile Arg Tyr Met Trp Ser Tyr	His Leu Ile Gly Leu Ile
170	175 180
Trp Thr Ser Glu Phe Ile Leu Ala Cys	Gln Gln Met Thr Ile Ala
185	190 195
Gly Ala Val Val Thr Cys Tyr Phe Asn	Arg Ser Lys Asn Asp Pro
200	205 210
Pro Asp His Pro Ile Leu Ser Ser Leu	Ser Ile Leu Phe Phe Tyr
215	220 225
His Gln Gly Thr Val Val Lys Gly Ser	Phe Leu Ile Ser Val Val
230	235 240
Arg Ile Pro Arg Ile Ile Val Met Tyr	Met Gln Asn Ala Leu Lys
245	250 255
Glu Gln Gln His Gly Ala Leu Ser Arg	Tyr Leu Phe Arg Cys Cys
260	265 270
Tyr Cys Cys Phe Trp Cys Leu Asp Lys	Tyr Leu Leu His Leu Asn
275	280 285
Gln Asn Ala Tyr Thr Thr Thr Ala Ile	Asn Gly Thr Asp Phe Cys
290	295 300
Thr Ser Ala Lys Asp Ala Phe Lys Ile	Leu Ser Lys Asn Ser Ser
305	310 315
His Phe Thr Ser Ile Asn Cys Phe Gly	Asp Phe Ile Ile Phe Leu
320	325 330
Gly Lys Val Leu Val Val Cys Phe Thr	Val Phe Gly Gly Leu Met
335	340 345
Ala Phe Asn Tyr Asn Arg Ala Phe Gln	Val Trp Ala Val Pro Leu
350	355 360
Leu Leu Val Ala Phe Phe Ala Tyr Leu	Val Ala His Ser Phe Leu
365	370 375
Ser Val Phe Glu Thr Val Leu Asp Ala	Leu Phe Leu Cys Phe Ala
380	385 390
Val Asp Leu Glu Thr Asn Asp Gly Ser	Ser Glu Lys Pro Tyr Phe
395	400 405
Met Asp Gln Glu Phe Leu Ser Phe Val	Lys Arg Ser Asn Lys Leu
410	415 420
Asn Asn Ala Arg Ala Gln Gln Asp Lys	His Ser Leu Arg Asn Glu
425	430 435
Glu Gly Thr Glu Leu Gln Ala Ile Val	Arg
440	445

<210> SEQ ID NO 33

<211> LENGTH: 2773

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 33

gttcgattag ctctctgag aagaagagaa aaggttcttg gacctctccc

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tgtttcttcc ttagaataat ttgtatggga tttgtgatgc aggaaagcct	100
aagggaaaaa gaatatcat tctgtgtggt gaaaattttt tgaaaaaaa	150
attgccttct tcaaacaagg gtgtcattct gatatttatg aggactgttg	200
ttctcactat gaaggcatct gttattgaaa tggtccttgt tttgctggtg	250
actggagtac attcaaaca agaaacggca aagaagatta aaaggcccaa	300
gttcaactgtg cctcagatca actgcgatgt caaagccgga aagatcatcg	350
atcctgagtt cattgtgaaa tgtccagcag gatgccaaga ccccaaatac	400
catgtttatg gcactgacgt gtatgcattc tactccagtg tgtgtggcgc	450
tgccgtacac agtgggtgtg ttgataatc aggagggaaa atacttggtc	500
ggaaggttg tggacagtct gggtacaaag ggagtattc caacgggtgc	550
caatcggtat ccctaccacg atggagagaa tccttttatcg tcttagaaag	600
taaacccaaa aagggtgtaa cctaccatc agctcttaca tactcatcat	650
cgaaggtcc agctgcccac gcaggtgaga ccacaaaagc ctatcagagg	700
ccacctattc cagggacaac tgcacagccg gtcactctga tgcagcttct	750
ggctgtcact gtagctgtgg ccacccccac caccttgcca aggccatccc	800
cttctgctgc ttctaccacc agcatcccca gaccacaatc agtgggccac	850
aggagccagg agatggatct ctgggccact gccacctaca caagcagcca	900
aaacaggccc agagctgac caggtatcca aaggcaagat ccttcaggag	950
ctgccttcca gaaacctgtt ggagcggatg tcagcctggg acttgttcca	1000
aaagaagaat tgagcacaca gtctttggag ccagtatccc tgggagatcc	1050
aaactgcaaa attgacttgt cgtttttaat tgatgggagc accagcattg	1100
gcaaacggcg attccgaatc cagaagcagc tcctggctga tgttgcccaa	1150
gctcttgaca ttggccctgc cgggtccactg atgggtgttg tccagtatgg	1200
agacaaccct gctactcact ttaacctcaa gacacacacg aattctcgag	1250
atctgaagac agccatagag aaaattactc agagaggagg actttctaatt	1300
gtaggtcggg ccatctcctt tgtgaccaag aacttctttt ccaaagccaa	1350
tggaaacaga agcggggctc ccaatgtggt ggtggtgatg gtggatggct	1400
ggcccacgga caaagtggag gaggttcaa gacttgcgag agatgcagga	1450
atcaacattt tcttcacac cattgaaggt gctgctgaaa atgagaagca	1500
gtatgtggtg gagcccaact ttgcaacaa ggccgtgtgc agaacaacg	1550
gcttctactc gctccacgtg cagagctggt ttggcctcca caagaccctg	1600
cagcctctgg tgaagcgggt ctgcgacact gaccgcctgg cctgcagcaa	1650
gacctgcttg aactcggctg acattggctt cgtcatcgac ggctccagca	1700
gtgtggggac gggcaacttc cgcacogtcc tccagtttgt gaccaacctc	1750
accaagagat ttgagatttc cgacacggac acgcgcatcg gggccgtgca	1800
gtacacctac gaacagcggc tggagtgttg gttcgacaag tacagcagca	1850
agcctgacat cctcaacgcc atcaagaggg tgggctactg gagtgggtggc	1900
accagcacgg gggctgcat caacttcgcc ctggagcagc tcttcaagaa	1950
gtccaagccc aacaagagga agttaatgat cctcatcacc gacgggaggt	2000

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cctacgacga cgtccggtac ccagccatgg ctgcccattct gaaggagtg	2050
atcacctatg cgataggcgt tgcctgggct gcccaagagg agctagaagt	2100
cattgccact caccgcgcca gagaccactc cttctttgtg gacgagtttg	2150
acaacctcca tcagtatgtc cccaggatca tccagaacat ttgtacagag	2200
ttcaactcac agcctcggaa ctgaattcag agcaggcaga gcaccagcaa	2250
gtgctgcttt actaactgac gtgttggaac accccaccgc ttaatggggc	2300
acgcacgggt catcaagtct tgggcagggc atggagaaac aaatgtcttg	2350
ttattattct ttgccatcat gctttttcat attccaaaac ttggagttac	2400
aaagatgatc aaaaacgtat agaattgacc aaaaggctac atcatgttga	2450
gggtgctgga gatttttacat ttgacaatt gttttcaaaa taaatgttcg	2500
gaatacagtg cagcccttac gacaggctta cgtagagctt ttgtgagatt	2550
tttaagtgtt tatttctgat ttgaactctg taaccctcag caagtttcat	2600
ttttgtcatg acaatgtagg aattgctgaa ttaaatgttt agaaggatga	2650
aaaaataaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2750
aaaaaaaaaa aaaaaaaaaa aag	2773

<210> SEQ ID NO 34

<211> LENGTH: 678

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 34

Met Arg Thr Val Val Leu Thr Met Lys Ala Ser Val Ile Glu Met	
1 5 10 15	
Phe Leu Val Leu Leu Val Thr Gly Val His Ser Asn Lys Glu Thr	
20 25 30	
Ala Lys Lys Ile Lys Arg Pro Lys Phe Thr Val Pro Gln Ile Asn	
35 40 45	
Cys Asp Val Lys Ala Gly Lys Ile Ile Asp Pro Glu Phe Ile Val	
50 55 60	
Lys Cys Pro Ala Gly Cys Gln Asp Pro Lys Tyr His Val Tyr Gly	
65 70 75	
Thr Asp Val Tyr Ala Ser Tyr Ser Ser Val Cys Gly Ala Ala Val	
80 85 90	
His Ser Gly Val Leu Asp Asn Ser Gly Gly Lys Ile Leu Val Arg	
95 100 105	
Lys Val Ala Gly Gln Ser Gly Tyr Lys Gly Ser Tyr Ser Asn Gly	
110 115 120	
Val Gln Ser Leu Ser Leu Pro Arg Trp Arg Glu Ser Phe Ile Val	
125 130 135	
Leu Glu Ser Lys Pro Lys Lys Gly Val Thr Tyr Pro Ser Ala Leu	
140 145 150	
Thr Tyr Ser Ser Ser Lys Ser Pro Ala Ala Gln Ala Gly Glu Thr	
155 160 165	
Thr Lys Ala Tyr Gln Arg Pro Pro Ile Pro Gly Thr Thr Ala Gln	
170 175 180	
Pro Val Thr Leu Met Gln Leu Leu Ala Val Thr Val Ala Val Ala	
185 190 195	

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Thr	Pro	Thr	Thr	Leu	Pro	Arg	Pro	Ser	Pro	Ser	Ala	Ala	Ser	Thr	200	205	210
Thr	Ser	Ile	Pro	Arg	Pro	Gln	Ser	Val	Gly	His	Arg	Ser	Gln	Glu	215	220	225
Met	Asp	Leu	Trp	Ser	Thr	Ala	Thr	Tyr	Thr	Ser	Ser	Gln	Asn	Arg	230	235	240
Pro	Arg	Ala	Asp	Pro	Gly	Ile	Gln	Arg	Gln	Asp	Pro	Ser	Gly	Ala	245	250	255
Ala	Phe	Gln	Lys	Pro	Val	Gly	Ala	Asp	Val	Ser	Leu	Gly	Leu	Val	260	265	270
Pro	Lys	Glu	Glu	Leu	Ser	Thr	Gln	Ser	Leu	Glu	Pro	Val	Ser	Leu	275	280	285
Gly	Asp	Pro	Asn	Cys	Lys	Ile	Asp	Leu	Ser	Phe	Leu	Ile	Asp	Gly	290	295	300
Ser	Thr	Ser	Ile	Gly	Lys	Arg	Arg	Phe	Arg	Ile	Gln	Lys	Gln	Leu	305	310	315
Leu	Ala	Asp	Val	Ala	Gln	Ala	Leu	Asp	Ile	Gly	Pro	Ala	Gly	Pro	320	325	330
Leu	Met	Gly	Val	Val	Gln	Tyr	Gly	Asp	Asn	Pro	Ala	Thr	His	Phe	335	340	345
Asn	Leu	Lys	Thr	His	Thr	Asn	Ser	Arg	Asp	Leu	Lys	Thr	Ala	Ile	350	355	360
Glu	Lys	Ile	Thr	Gln	Arg	Gly	Gly	Leu	Ser	Asn	Val	Gly	Arg	Ala	365	370	375
Ile	Ser	Phe	Val	Thr	Lys	Asn	Phe	Phe	Ser	Lys	Ala	Asn	Gly	Asn	380	385	390
Arg	Ser	Gly	Ala	Pro	Asn	Val	Val	Val	Val	Met	Val	Asp	Gly	Trp	395	400	405
Pro	Thr	Asp	Lys	Val	Glu	Glu	Ala	Ser	Arg	Leu	Ala	Arg	Glu	Ser	410	415	420
Gly	Ile	Asn	Ile	Phe	Phe	Ile	Thr	Ile	Glu	Gly	Ala	Ala	Glu	Asn	425	430	435
Glu	Lys	Gln	Tyr	Val	Val	Glu	Pro	Asn	Phe	Ala	Asn	Lys	Ala	Val	440	445	450
Cys	Arg	Thr	Asn	Gly	Phe	Tyr	Ser	Leu	His	Val	Gln	Ser	Trp	Phe	455	460	465
Gly	Leu	His	Lys	Thr	Leu	Gln	Pro	Leu	Val	Lys	Arg	Val	Cys	Asp	470	475	480
Thr	Asp	Arg	Leu	Ala	Cys	Ser	Lys	Thr	Cys	Leu	Asn	Ser	Ala	Asp	485	490	495
Ile	Gly	Phe	Val	Ile	Asp	Gly	Ser	Ser	Ser	Val	Gly	Thr	Gly	Asn	500	505	510
Phe	Arg	Thr	Val	Leu	Gln	Phe	Val	Thr	Asn	Leu	Thr	Lys	Glu	Phe	515	520	525
Glu	Ile	Ser	Asp	Thr	Asp	Thr	Arg	Ile	Gly	Ala	Val	Gln	Tyr	Thr	530	535	540
Tyr	Glu	Gln	Arg	Leu	Glu	Phe	Gly	Phe	Asp	Lys	Tyr	Ser	Ser	Lys	545	550	555
Pro	Asp	Ile	Leu	Asn	Ala	Ile	Lys	Arg	Val	Gly	Tyr	Trp	Ser	Gly	560	565	570
Gly	Thr	Ser	Thr	Gly	Ala	Ala	Ile	Asn	Phe	Ala	Leu	Glu	Gln	Leu	575	580	585
Phe	Lys	Lys	Ser	Lys	Pro	Asn	Lys	Arg	Lys	Leu	Met	Ile	Leu	Ile			

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590					595					600				
Thr	Asp	Gly	Arg	Ser	Tyr	Asp	Asp	Val	Arg	Ile	Pro	Ala	Met	Ala
				605					610					615
Ala	His	Leu	Lys	Gly	Val	Ile	Thr	Tyr	Ala	Ile	Gly	Val	Ala	Trp
				620					625					630
Ala	Ala	Gln	Glu	Glu	Leu	Glu	Val	Ile	Ala	Thr	His	Pro	Ala	Arg
				635					640					645
Asp	His	Ser	Phe	Phe	Val	Asp	Glu	Phe	Asp	Asn	Leu	His	Gln	Tyr
				650					655					660
Val	Pro	Arg	Ile	Ile	Gln	Asn	Ile	Cys	Thr	Glu	Phe	Asn	Ser	Gln
				665					670					675

Pro Arg Asn

<210> SEQ ID NO 35

<211> LENGTH: 2095

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 35

ccgagcacag gagattgcct gcgttttagga ggtggctgcg ttgtgggaaa	50
agctatcaag gaagaaattg ccaaaccatg tcttttttctc tgttttcaga	100
gtagttcaca acagatctga gtgttttaaat taagcatgga atacagaaaa	150
caacaaaaaa cttaagcttt aatttcatct ggaattccac agttttctta	200
gctccctgga cccggttgac ctgttggtctc ttcccgctgg ctgctctatc	250
acgtggtgct ctccgactac tcaccccgag tgtaaagaac cttcggtctg	300
cggtcttctg agctgctgtg gatggcctcg gctctctgga ctgtccttcc	350
gagtaggatg tcaactgagat ccctcaaagt gagcctcctg ctgctgtcac	400
tcctgagttt ctttgtgatg tggtaacctc gccttcccca ctacaatgtg	450
atagaacgcg tgaactggat gtacttctat gagtatgagc cgattttacag	500
acaagacttt cacttcacac ttcgagagca ttcaaactgc tctcatcaaa	550
atccatttct ggtcattctg gtgacctccc acccttcaga tgtgaaagcc	600
aggcaggcca ttagagttac ttgggggtgaa aaaaagtctt ggtggggata	650
tgaggttctt acatttttct tattaggcca agaggctgaa aaggaagaca	700
aaatgttggc attgtcctta gaggatgaac accttcttta tggtgacata	750
atccgacaag atttttttaga cacatataat aacctgacct tgaaaaccat	800
tatggcattc aggtgggtaa ctgagttttg cccaatgcc aagtacgtaa	850
tgaagacaga cactgatgtt ttcataaata ctggcaattt agtgaagtat	900
cttttaaacc taaaccactc agagaagttt ttcacaggtt atcctctaatt	950
tgataattat tcctatagag gattttacca aaaaacccat atttcttacc	1000
aggagtatcc tttcaagggt ttccctccat actgcagtgg gttgggttat	1050
ataatgtcca gagatttggg gcccaaggatc tatgaaatga tgggtcacgt	1100
aaaacccatc aagtttgaag atgtttatgt cgggatctgt ttgaatttat	1150
taaaagtga catcatatt ccagaagaca caaatctttt ctttctatat	1200
agaatccatt tggatgtctg tcaactgaga cgtgtgattg cagcccatgg	1250
cttttcttcc aaggagatca tcactttttg gcaggatcatg ctaaggaaca	1300

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ccacatgcc	ttattaacct	cacattctac	aaaaagccta	gaaggacagg	1350
ataccttg	gaaagtgtta	aataaagtag	gtactgtgga	aaattcatgg	1400
ggaggtcagt	gtgctggcct	acactgaact	gaaactcatg	aaaaaccag	1450
actggagact	ggagggttac	acttgtgatt	tattagtcag	gcccttcaaa	1500
gatgatattg	ggaggaatta	aataaaagg	aattggaggt	ttttgctaaa	1550
gaaattaata	ggaccaaaca	atttgacat	gtcattctgt	agactagaat	1600
ttcttaaaag	ggtgttactg	agttataagc	tcactaggct	gtaaaaacaa	1650
aacaatgtag	agttttat	attgaacaat	gtagtcactt	gaaggttttg	1700
tgtatatctt	atgtggatta	ccaattttaa	aatatatgta	gttctgtgtc	1750
aaaaaacttc	ttcactgaag	ttatactgaa	caaaatttta	cctgtttttg	1800
gtcatttata	aagtacttca	agatgttgca	gtatttcaca	gttattatta	1850
tttaaaatta	cttcaacttt	gtgtttttaa	atgttttgac	gatttcaata	1900
caagataaaa	aggatagtga	atcattcttt	acatgcaaac	attttccagt	1950
tacttaactg	atcagtttat	tattgataca	tcactccatt	aatgtaaagt	2000
cataggtcat	tattgcatat	cagtaatctc	ttggactttg	ttaaatattt	2050
tactgtggta	atatagagaa	gaattaaagc	aagaaaatct	gaaaa	2095

<210> SEQ ID NO 36

<211> LENGTH: 331

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 36

Met	Ala	Ser	Ala	Leu	Trp	Thr	Val	Leu	Pro	Ser	Arg	Met	Ser	Leu
1				5					10					15
Arg	Ser	Leu	Lys	Trp	Ser	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Ser	Phe
				20					25					30
Phe	Val	Met	Trp	Tyr	Leu	Ser	Leu	Pro	His	Tyr	Asn	Val	Ile	Glu
				35					40					45
Arg	Val	Asn	Trp	Met	Tyr	Phe	Tyr	Glu	Tyr	Glu	Pro	Ile	Tyr	Arg
				50					55					60
Gln	Asp	Phe	His	Phe	Thr	Leu	Arg	Glu	His	Ser	Asn	Cys	Ser	His
				65					70					75
Gln	Asn	Pro	Phe	Leu	Val	Ile	Leu	Val	Thr	Ser	His	Pro	Ser	Asp
				80					85					90
Val	Lys	Ala	Arg	Gln	Ala	Ile	Arg	Val	Thr	Trp	Gly	Glu	Lys	Lys
				95					100					105
Ser	Trp	Trp	Gly	Tyr	Glu	Val	Leu	Thr	Phe	Phe	Leu	Leu	Gly	Gln
				110					115					120
Glu	Ala	Glu	Lys	Glu	Asp	Lys	Met	Leu	Ala	Leu	Ser	Leu	Glu	Asp
				125					130					135
Glu	His	Leu	Leu	Tyr	Gly	Asp	Ile	Ile	Arg	Gln	Asp	Phe	Leu	Asp
				140					145					150
Thr	Tyr	Asn	Asn	Leu	Thr	Leu	Lys	Thr	Ile	Met	Ala	Phe	Arg	Trp
				155					160					165
Val	Thr	Glu	Phe	Cys	Pro	Asn	Ala	Lys	Tyr	Val	Met	Lys	Thr	Asp
				170					175					180
Thr	Asp	Val	Phe	Ile	Asn	Thr	Gly	Asn	Leu	Val	Lys	Tyr	Leu	Leu
				185					190					195

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Asn	Leu	Asn	His	Ser	Glu	Lys	Phe	Phe	Thr	Gly	Tyr	Pro	Leu	Ile
				200					205					210
Asp	Asn	Tyr	Ser	Tyr	Arg	Gly	Phe	Tyr	Gln	Lys	Thr	His	Ile	Ser
				215					220					225
Tyr	Gln	Glu	Tyr	Pro	Phe	Lys	Val	Phe	Pro	Pro	Tyr	Cys	Ser	Gly
				230					235					240
Leu	Gly	Tyr	Ile	Met	Ser	Arg	Asp	Leu	Val	Pro	Arg	Ile	Tyr	Glu
				245					250					255
Met	Met	Gly	His	Val	Lys	Pro	Ile	Lys	Phe	Glu	Asp	Val	Tyr	Val
				260					265					270
Gly	Ile	Cys	Leu	Asn	Leu	Leu	Lys	Val	Asn	Ile	His	Ile	Pro	Glu
				275					280					285
Asp	Thr	Asn	Leu	Phe	Phe	Leu	Tyr	Arg	Ile	His	Leu	Asp	Val	Cys
				290					295					300
Gln	Leu	Arg	Arg	Val	Ile	Ala	Ala	His	Gly	Phe	Ser	Ser	Lys	Glu
				305					310					315
Ile	Ile	Thr	Phe	Trp	Gln	Val	Met	Leu	Arg	Asn	Thr	Thr	Cys	His
				320					325					330

Tyr

<210> SEQ ID NO 37
 <211> LENGTH: 2846
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 37

cgctcgggca ccagccgcgg caaggatgga gctggggtgc tggacgcagt	50
tggggctcac ttttcttcag ctccttctca tctcgtcctt gccaaagagag	100
tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg	150
tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga	200
gggaagtcgt ggggtataacc atcccttgct gcaggaatga ggagaatgag	250
tgtgactcct gcctgatcca ccaggttgt accatctttg aaaactgcaa	300
gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga	350
aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc	400
atgcatgtg gccaggttct gcgagcccca aagggtcaga tttgttgga	450
aagctatccc ctaaatgctc actgtgaatg gaccattcat gctaaacctg	500
ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac	550
atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcatgg	600
ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga	650
gcataggatc ctactccac gtcctcttcc actccgatgg ctccaagaat	700
tttgacgggt tccatgccat ttatgaggag atcacagcat gtcctcatc	750
cccttgtttc catgacggca cgtgcgtcct tgacaaggct ggtctttaca	800
agtgtgcctg cttggcaggc tatactgggc agcgtgtgta aaatctcctt	850
gaagaaagaa actgctcaga ccctgggggc ccagtcaatg ggtaccagaa	900
aataacaggg ggccctgggc ttatcaacgg acgccatgct aaaattggca	950
ccgtggtgtc tttcttttgt aacaactcct atgttcttag tggcaatgag	1000
aaaagaactt gccagcagaa tggagagtgg tcagggaac agcccatctg	1050

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cataaaaagcc tgccgagaac caaagatttc agacctggtg agaaggagag	1100
ttcttccgat gcaggttcag tcaagggaga caccattaca ccagctatac	1150
tcagcggcct tcagcaagca gaaactgcag agtgccccta ccaagaagcc	1200
agcccttccc ttggagatc tgcccatggg ataccaacat ctgcataccc	1250
agctccagta tgagtgcac tcacccttct accgccgcct gggcagcagc	1300
aggaggacat gtctgaggac tgggaagtgg agtgggctgg caccatcctg	1350
catccctatc tgcgggaaaa ttgagaacat cactgctcca aagaccaag	1400
ggttgcgctg gccgtggcag gcagccatct acaggaggac cagcggggtg	1450
catgacggca gcctacacaa gggagcgtgg ttcctagtct gcagcgggtc	1500
cctggagaat gagcgcactg tgggtggggc tgcccactgt gttactgacc	1550
tggggaaggt caccatgatc aagacagcag acctgaaagt tgttttgggg	1600
aaattctacc gggatgatga ccgggatgag aagaccatcc agagcctaca	1650
gattttctgt atcattctgc atcccaacta tgaccccatc ctgcttgatg	1700
ctgacatcgc catcctgaag ctccctagaca aggcccgatc cagcaccga	1750
gtccagccca tctgcctcgc tgccagtcgg gatctcagca cttccttcca	1800
ggagtccca atcactgtgg ctggctggaa tgccttgga gacgtgagga	1850
gccctggcct caagaacgac aactgcgcct ctgggggtgt cagtgtggtg	1900
gactcgtcgc tgtgtgagga gcagcatgag gaccatggca tcccagtga	1950
tgtcactgat aacatgttct gtgccagctg ggaaccact gcccttctg	2000
atatctgcac tgcagagaca ggaggcatcg cggctgtgtc cttcccgga	2050
cgagcatctc ctgagccacg ctggcatctg atgggactgg tcagctggag	2100
ctatgataaa acatgcagcc acaggctctc cactgccttc accaaggtgc	2150
tgccttttaa agactggatt gaaagaaata tgaaatgaac catgctcatg	2200
cactccttga gaagtgttct tgtatatccg tctgtacgtg tgtcattgcg	2250
tgaagcagtg tgggcctgaa gtgtgatttg gcctgtgaac ttggctgtgc	2300
cagggttct gacttcaggg acaaaactca gtgaagggtg agtagacctc	2350
cattgctggt aggtgatgc cgcgtccact actaggacag ccaattggaa	2400
gatgccaggg cttgcaagaa gtaagtttct tcaaagaaga ccatatacaa	2450
aacctctcca ctccactgac ctggtggtct tcccactt tcagttatac	2500
gaatgccatc agcttgacca ggaagatct gggcttcatg agggccctt	2550
tgaggctctc aagttctaga gagctgcctg tgggacagcc cagggcagca	2600
gagctgggat gtggtgcatg cctttgtgta catggccaca gtacagtctg	2650
gtccttttcc ttcccatct cttgtacaca ttttaataaa ataagggttg	2700
gcttctgaac tacaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2750
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2800
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa	2846

<210> SEQ ID NO 38

<211> LENGTH: 720

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 38

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Met	Glu	Leu	Gly	Cys	Trp	Thr	Gln	Leu	Gly	Leu	Thr	Phe	Leu	Gln	1	5	10	15
Leu	Leu	Leu	Ile	Ser	Ser	Leu	Pro	Arg	Glu	Tyr	Thr	Val	Ile	Asn	20	25	30	
Glu	Ala	Cys	Pro	Gly	Ala	Glu	Trp	Asn	Ile	Met	Cys	Arg	Glu	Cys	35	40	45	
Cys	Glu	Tyr	Asp	Gln	Ile	Glu	Cys	Val	Cys	Pro	Gly	Lys	Arg	Glu	50	55	60	
Val	Val	Gly	Tyr	Thr	Ile	Pro	Cys	Cys	Arg	Asn	Glu	Glu	Asn	Glu	65	70	75	
Cys	Asp	Ser	Cys	Leu	Ile	His	Pro	Gly	Cys	Thr	Ile	Phe	Glu	Asn	80	85	90	
Cys	Lys	Ser	Cys	Arg	Asn	Gly	Ser	Trp	Gly	Gly	Thr	Leu	Asp	Asp	95	100	105	
Phe	Tyr	Val	Lys	Gly	Phe	Tyr	Cys	Ala	Glu	Cys	Arg	Ala	Gly	Trp	110	115	120	
Tyr	Gly	Gly	Asp	Cys	Met	Arg	Cys	Gly	Gln	Val	Leu	Arg	Ala	Pro	125	130	135	
Lys	Gly	Gln	Ile	Leu	Leu	Glu	Ser	Tyr	Pro	Leu	Asn	Ala	His	Cys	140	145	150	
Glu	Trp	Thr	Ile	His	Ala	Lys	Pro	Gly	Phe	Val	Ile	Gln	Leu	Arg	155	160	165	
Phe	Val	Met	Leu	Ser	Leu	Glu	Phe	Asp	Tyr	Met	Cys	Gln	Tyr	Asp	170	175	180	
Tyr	Val	Glu	Val	Arg	Asp	Gly	Asp	Asn	Arg	Asp	Gly	Gln	Ile	Ile	185	190	195	
Lys	Arg	Val	Cys	Gly	Asn	Glu	Arg	Pro	Ala	Pro	Ile	Gln	Ser	Ile	200	205	210	
Gly	Ser	Ser	Leu	His	Val	Leu	Phe	His	Ser	Asp	Gly	Ser	Lys	Asn	215	220	225	
Phe	Asp	Gly	Phe	His	Ala	Ile	Tyr	Glu	Glu	Ile	Thr	Ala	Cys	Ser	230	235	240	
Ser	Ser	Pro	Cys	Phe	His	Asp	Gly	Thr	Cys	Val	Leu	Asp	Lys	Ala	245	250	255	
Gly	Ser	Tyr	Lys	Cys	Ala	Cys	Leu	Ala	Gly	Tyr	Thr	Gly	Gln	Arg	260	265	270	
Cys	Glu	Asn	Leu	Leu	Glu	Glu	Arg	Asn	Cys	Ser	Asp	Pro	Gly	Gly	275	280	285	
Pro	Val	Asn	Gly	Tyr	Gln	Lys	Ile	Thr	Gly	Gly	Pro	Gly	Leu	Ile	290	295	300	
Asn	Gly	Arg	His	Ala	Lys	Ile	Gly	Thr	Val	Val	Ser	Phe	Phe	Cys	305	310	315	
Asn	Asn	Ser	Tyr	Val	Leu	Ser	Gly	Asn	Glu	Lys	Arg	Thr	Cys	Gln	320	325	330	
Gln	Asn	Gly	Glu	Trp	Ser	Gly	Lys	Gln	Pro	Ile	Cys	Ile	Lys	Ala	335	340	345	
Cys	Arg	Glu	Pro	Lys	Ile	Ser	Asp	Leu	Val	Arg	Arg	Arg	Val	Leu	350	355	360	
Pro	Met	Gln	Val	Gln	Ser	Arg	Glu	Thr	Pro	Leu	His	Gln	Leu	Tyr	365	370	375	
Ser	Ala	Ala	Phe	Ser	Lys	Gln	Lys	Leu	Gln	Ser	Ala	Pro	Thr	Lys	380	385	390	

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Lys	Pro	Ala	Leu	Pro	Phe	Gly	Asp	Leu	Pro	Met	Gly	Tyr	Gln	His
			395						400					405
Leu	His	Thr	Gln	Leu	Gln	Tyr	Glu	Cys	Ile	Ser	Pro	Phe	Tyr	Arg
			410						415					420
Arg	Leu	Gly	Ser	Ser	Arg	Arg	Thr	Cys	Leu	Arg	Thr	Gly	Lys	Trp
			425						430					435
Ser	Gly	Arg	Ala	Pro	Ser	Cys	Ile	Pro	Ile	Cys	Gly	Lys	Ile	Glu
			440						445					450
Asn	Ile	Thr	Ala	Pro	Lys	Thr	Gln	Gly	Leu	Arg	Trp	Pro	Trp	Gln
			455						460					465
Ala	Ala	Ile	Tyr	Arg	Arg	Thr	Ser	Gly	Val	His	Asp	Gly	Ser	Leu
			470						475					480
His	Lys	Gly	Ala	Trp	Phe	Leu	Val	Cys	Ser	Gly	Ala	Leu	Val	Asn
			485						490					495
Glu	Arg	Thr	Val	Val	Val	Ala	Ala	His	Cys	Val	Thr	Asp	Leu	Gly
			500						505					510
Lys	Val	Thr	Met	Ile	Lys	Thr	Ala	Asp	Leu	Lys	Val	Val	Leu	Gly
			515						520					525
Lys	Phe	Tyr	Arg	Asp	Asp	Asp	Arg	Asp	Glu	Lys	Thr	Ile	Gln	Ser
			530						535					540
Leu	Gln	Ile	Ser	Ala	Ile	Ile	Leu	His	Pro	Asn	Tyr	Asp	Pro	Ile
			545						550					555
Leu	Leu	Asp	Ala	Asp	Ile	Ala	Ile	Leu	Lys	Leu	Leu	Asp	Lys	Ala
			560						565					570
Arg	Ile	Ser	Thr	Arg	Val	Gln	Pro	Ile	Cys	Leu	Ala	Ala	Ser	Arg
			575						580					585
Asp	Leu	Ser	Thr	Ser	Phe	Gln	Glu	Ser	His	Ile	Thr	Val	Ala	Gly
			590						595					600
Trp	Asn	Val	Leu	Ala	Asp	Val	Arg	Ser	Pro	Gly	Phe	Lys	Asn	Asp
			605						610					615
Thr	Leu	Arg	Ser	Gly	Val	Val	Ser	Val	Val	Asp	Ser	Leu	Leu	Cys
			620						625					630
Glu	Glu	Gln	His	Glu	Asp	His	Gly	Ile	Pro	Val	Ser	Val	Thr	Asp
			635						640					645
Asn	Met	Phe	Cys	Ala	Ser	Trp	Glu	Pro	Thr	Ala	Pro	Ser	Asp	Ile
			650						655					660
Cys	Thr	Ala	Glu	Thr	Gly	Gly	Ile	Ala	Ala	Val	Ser	Phe	Pro	Gly
			665						670					675
Arg	Ala	Ser	Pro	Glu	Pro	Arg	Trp	His	Leu	Met	Gly	Leu	Val	Ser
			680						685					690
Trp	Ser	Tyr	Asp	Lys	Thr	Cys	Ser	His	Arg	Leu	Ser	Thr	Ala	Phe
			695						700					705
Thr	Lys	Val	Leu	Pro	Phe	Lys	Asp	Trp	Ile	Glu	Arg	Asn	Met	Lys
			710						715					720

<210> SEQ ID NO 39

<211> LENGTH: 2571

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 39

ggttcctaca tcctctcattc tgagaatcag agagcataat cttcttacgg	50
gcccgtgatt tattaacgtg gcttaattctg aaggtttctca gtcaaatctt	100
ttgtgatcta ctgattgtgg gggcatggca aggtttgctt aaaggagctt	150

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ggctggtttg	ggcccttgta	gctgacagaa	ggtggccagg	gagaatgcag	200
cacactgctc	ggagaatgaa	ggcgcttctg	ttgctggtct	tgctttggct	250
cagtctgtct	aactacattg	acaatgtggg	caacctgcac	ttcctgtatt	300
cagaactctg	taaaggtgcc	tcccactacg	gcctgaccaa	agataggaa	350
aggcgctcac	aagatggctg	tccagacggc	tgtgcgagcc	tcacagccac	400
ggctccctcc	ccagagggtt	ctgcagctgc	cacctctccc	ttaatgacag	450
acgagcctgg	cctagacaac	cctgcctacg	tgtcctcggc	agaggacggg	500
cagccagcaa	tcagcccagt	ggactctggc	cggagcaacc	gaactagggc	550
acggcccttt	gagagatcca	ctattagaag	cagatcattt	aaaaaataa	600
atcgagcttt	gagtgttctt	cgaaggacaa	agagcgggag	tgacgttgcc	650
aacctgccc	accagggcag	ggaaaattct	gaaaacacca	ctgcccctga	700
agtctttcca	aggttggtacc	acctgattcc	agatgggtgaa	attaccagca	750
tcaagatcaa	tcgagtagat	cccagtgaaa	gcctctctat	taggctgggtg	800
ggaggtagcg	aaacccact	ggtccatctc	attatccaac	acatttatcg	850
tgatgggggtg	atcgccagag	acggccggct	actgccagga	gacatcattc	900
taaaggtcaa	cgggatggac	atcagcaatg	tccctcacia	ctacgctgtg	950
cgtctctctg	ggcagccctg	ccaggtgctg	tggtgactg	tgatgcgtga	1000
acagaagttc	cgcagcagga	acaatggaca	ggccccgat	gcctacagac	1050
cccagatga	cagctttcat	gtgattctca	acaaaagtag	cccagaggag	1100
cagcttgtaa	taaaactggt	gcgcaagggt	gatgagcctg	gggttttcat	1150
cttcaatgtg	ctggatggcg	gtgtggcata	tcgacatggt	cagcttgagg	1200
agaatgaccg	tgtgttagcc	atcaatggac	atgatcttcg	atatggcagc	1250
ccagaaagt	cggctcatct	gattcaggcc	agtgaagac	gtgttcacct	1300
cgtcgtgtcc	cgccagggtc	ggcagcggag	ccctgacatc	tttcagggaag	1350
ccggctggaa	cagcaatggc	agctgggtccc	cagggccagg	ggagaggagc	1400
aacactccca	agccctccca	tcctacaatt	acttgtcatg	agaagggtgt	1450
aaatatccaa	aaagaccccg	gtgaatctct	cggcatgacc	gtcgcagggg	1500
gagcatcaca	tagagaatgg	gatttgcta	tctatgtcat	cagtgttgag	1550
cccggaggag	tcataagcag	agatggaaga	ataaaaacag	gtgacatttt	1600
gttgaatgtg	gatggggctg	aactgacaga	ggtcagccgg	agtgagcag	1650
tggcattatt	gaaaagaaca	tcactctcga	tagtactcaa	agctttggaa	1700
gtcaaagagt	atgagcccca	ggaagactgc	agcagcccag	cagccctgga	1750
ctccaaccac	aacatggccc	caccagtgga	ctggtcccca	tcctgggtca	1800
tgtggctgga	attaccacgg	tgcttgata	actgtaaaga	tattgtatta	1850
cgaagaaaca	cagctggaag	tctgggcttc	tgcatgttag	gaggttatga	1900
agaatacaat	ggaaacaaac	cttttttcat	caaattccatt	gttgaaggaa	1950
caccagcata	caatgatgga	agaattagat	gtggtgatat	tcttcttgct	2000
gtcaatggta	gaagtacatc	aggaatgata	catgcttgct	tggaagact	2050
gctgaaagaa	cttaaaggaa	gaattactct	aactattggt	tcttggcctg	2100

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gcactttttt atagaatcaa tgatgggtca gagaaaaaca gaaaaatcac	2150
aaataggcta agaagttgaa acactatatt tatcttgtca gtttttatat	2200
ttaaagaaag aatacattgt aaaaatgtca ggaaaagtat gatcatctaa	2250
tgaaagccag ttacacctca gaaaatatga ttccaaaaaa attaaaacta	2300
ctagtttttt ttcagtggtg aggattttctc attactctac aacattgttt	2350
atattttttc tattcaataa aaagccctaa aacaactaaa atgattgatt	2400
tgtatacccc actgaattca agctgattta aatttaaaat ttggtatatg	2450
ctgaagtctg ccaagggtag attatggcca tttttaattt acagctaaaa	2500
tattttttta aatgcattgc tgagaaacgt tgctttcatc aaacaagaat	2550
aaatattttt cagaagttaa a	2571

<210> SEQ ID NO 40

<211> LENGTH: 632

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 40

Met Lys Ala Leu Leu Leu Val Leu Pro Trp Leu Ser Pro Ala	
1 5 10 15	
Asn Tyr Ile Asp Asn Val Gly Asn Leu His Phe Leu Tyr Ser Glu	
20 25 30	
Leu Cys Lys Gly Ala Ser His Tyr Gly Leu Thr Lys Asp Arg Lys	
35 40 45	
Arg Arg Ser Gln Asp Gly Cys Pro Asp Gly Cys Ala Ser Leu Thr	
50 55 60	
Ala Thr Ala Pro Ser Pro Glu Val Ser Ala Ala Ala Thr Ile Ser	
65 70 75	
Leu Met Thr Asp Glu Pro Gly Leu Asp Asn Pro Ala Tyr Val Ser	
80 85 90	
Ser Ala Glu Asp Gly Gln Pro Ala Ile Ser Pro Val Asp Ser Gly	
95 100 105	
Arg Ser Asn Arg Thr Arg Ala Arg Pro Phe Glu Arg Ser Thr Ile	
110 115 120	
Arg Ser Arg Ser Phe Lys Lys Ile Asn Arg Ala Leu Ser Val Leu	
125 130 135	
Arg Arg Thr Lys Ser Gly Ser Ala Val Ala Asn His Ala Asp Gln	
140 145 150	
Gly Arg Glu Asn Ser Glu Asn Thr Thr Ala Pro Glu Val Phe Pro	
155 160 165	
Arg Leu Tyr His Leu Ile Pro Asp Gly Glu Ile Thr Ser Ile Lys	
170 175 180	
Ile Asn Arg Val Asp Pro Ser Glu Ser Leu Ser Ile Arg Leu Val	
185 190 195	
Gly Gly Ser Glu Thr Pro Leu Val His Ile Ile Ile Gln His Ile	
200 205 210	
Tyr Arg Asp Gly Val Ile Ala Arg Asp Gly Arg Leu Leu Pro Gly	
215 220 225	
Asp Ile Ile Leu Lys Val Asn Gly Met Asp Ile Ser Asn Val Pro	
230 235 240	
His Asn Tyr Ala Val Arg Leu Leu Arg Gln Pro Cys Gln Val Leu	
245 250 255	

<210> SEQ ID NO 41

-continued

<211> LENGTH: 1964

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 41

accaggcatt gtatcttcag ttgtcatcaa gttcgcaatc agattggaaa	50
agctcaactt gaagctttct tgcctgcagt gaagcagaga gatagatatt	100
attcacgtaa taaaaaacat gggcttcaac ctgactttcc acctttccta	150
caaatccga ttactgttgc tgttgacttt gtgcctgaca gtggttgggt	200
gggccaccag taactacttc gtgggtgccca ttcaagagat tcctaaagca	250
aaggagtcca tggctaattt ccataagacc ctcatcttgg ggaagggaaa	300
aactctgact aatgaagcat ccacgaagaa ggtagaactt gacaactgtc	350
cttctgtgtc tccttacctc agaggccaga gcaagctcat tttcaaacca	400
gatctcactt tggaagaggt acaggcagaa aatcccaaag tgtccagagg	450
ccggtatcgc cctcaggaat gtaaagcttt acagagggtc gccatcctcg	500
ttccccaccg gaacagagag aaacacctga tgtacctgct ggaacatctg	550
catcccttcc tgcagaggca gcagctggat tatggcatct acgtcatcca	600
ccaggctgaa ggtaaaaagt ttaatcgagc caaactcttg aatgtgggct	650
atctagaagc cctcaaggaa gaaaattggg actgctttat attccacgat	700
gtggacctgg taccgcagaa tgactttaac ctttacaagt gtgaggagca	750
tccccagcat ctggtggttg gcaggaacag cactgggtac aggttacgtt	800
acagtggata ttttgggggt gttactgccc taagcagaga gcagtttttc	850
aagggtaatg gattctctaa caactactgg ggatggggag gcgaagacga	900
tgacctcaga ctcagggttg agctccaaag aatgaaaatt tcccggcccc	950
tgctgaagt gggtaaatat acaatggtct tccacactag agacaaaggc	1000
aatgaggtga acgcagaacg gatgaagctc ttacaccaag tgtcacgagt	1050
ctggagaaca gatgggttga gtagtgttc ttataaatta gtatctgtgg	1100
aacacaatcc tttatatatc aacatcacag tggatttctg gtttgggtga	1150
tgacctgga tcttttggg atgtttggaa gaactgattc tttgtttgca	1200
ataattttgg cctagagact tcaaatagta gcacacatta agaacctgtt	1250
acagctcatt gttgagctga atttttcctt tttgtatttt cttagcagag	1300
ctcctggtga tgtagagtat aaaacagttg taacaagaca gctttcttag	1350
tcattttgat catgagggtt aaatatgta atatggatac ttgaaggact	1400
ttatataaaa ggatgactca aaggataaaa tgaacgctat ttgaggactc	1450
tggttgaaag agattttatt aaatttgaag taatatatta tgggataaaa	1500
ggccacagga aataagactg ctgaatgtct gagagaacca gagttgttct	1550
cgtccaaggt agaaaggtag gaagatacaa tactgttatt catttatcct	1600
gtacaatcat ctgtgaagt gtggtgtcag gtgagaaggc gtccacaaaa	1650
gaggggagaa aaggcgacga atcaggacac agtgaacttg ggaatgaaga	1700
ggtagcagga ggggtggagt tcggctgcaa aggcagcagt agctgagctg	1750
gttgacaggt ctgatagcct tcaggggagg acctgcccag gtatgccttc	1800
cagtgatgcc caccagagaa tacattctct attagttttt aaagagtttt	1850

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tgtaaaatga ttttgtacaa gtaggatatg aattagcagt ttacaagttt	1900
acatatataac taataataaa tatgtctatc aaatacctct gtagtaaaat	1950
gtgaaaaagc aaaa	1964

<210> SEQ ID NO 42
 <211> LENGTH: 344
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 42

Met	Gly	Phe	Asn	Leu	Thr	Phe	His	Leu	Ser	Tyr	Lys	Phe	Arg	Leu	
1				5					10					15	
Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr	
				20					25					30	
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys	
				35					40					45	
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly	
				50					55					60	
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp	
				65					70					75	
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu	
				80					85					90	
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn	
				95					100					105	
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala	
				110					115					120	
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys	
				125					130					135	
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg	
				140					145					150	
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly	
				155					160					165	
Lys	Lys	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu	
				170					175					180	
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val	
				185					190					195	
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu	
				200					205					210	
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg	
				215					220					225	
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg	
				230					235					240	
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly	
				245					250					255	
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Gln	
				260					265					270	
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr	
				275					280					285	
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu	
				290					295					300	
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp	
				305					310					315	
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn	

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320	325	330	
Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala			
335	340		
 <210> SEQ ID NO 43			
<211> LENGTH: 485			
<212> TYPE: DNA			
<213> ORGANISM: Homo Sapien			
 <400> SEQUENCE: 43			
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga		50	
gctcccagat ctggggccgct tgccctcctgc tctcctcctc cctcgccagc		100	
ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct		150	
gcaaccccgag gacagagctg gagccagggc cagctggatg cccatgttcc		200	
agaggcgaag gaggcgagac acccacttcc ccatctgcat tttctgctgc		250	
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct		300	
acctgccctg ccccgctccc ctcccttctc tatttattcc tgctgccccca		350	
gaacataggt cttggaataa aatggctggt tcttttgttt tccaaaaaaa		400	
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa		450	
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa		485	
 <210> SEQ ID NO 44			
<211> LENGTH: 84			
<212> TYPE: PRT			
<213> ORGANISM: Homo Sapien			
 <400> SEQUENCE: 44			
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu			
1 5 10 15			
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln			
20 25 30			
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala			
35 40 45			
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp			
50 55 60			
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg			
65 70 75			
Ser Lys Cys Gly Met Cys Cys Lys Thr			
80			
 <210> SEQ ID NO 45			
<211> LENGTH: 1076			
<212> TYPE: DNA			
<213> ORGANISM: Homo Sapien			
 <400> SEQUENCE: 45			
gtggcttcat ttcagtggct gacttocaga gagcaatatg gctggttccc		50	
caacatgcct caccctcatc tatatccttt ggcagctcac agggtcagca		100	
gcctctggac ccgtgaaaga gctggtcggt tccgttggtg gggccgtgac		150	
tttccccctg aagtccaaag taaagcaagt tgactctatt gtctggacct		200	
tcaacacaac ccctcttgtc accatacagc cagaaggggg cactatcata		250	
gtgacccaaa atcgtaatag ggagagagta gacttcccag atggaggcta		300	

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ctccctgaag ctcagcaaac tgaagaagaa tgactcaggg atctactatg	350
tggggatata cagctcatca ctccagcagc cctccaccca ggagtacgtg	400
ctgcatgtct acgagcacct gtcaaagcct aaagtcacca tgggtctgca	450
gagcaataag aatggcacct gtgtgaccaa tctgacatgc tgcattggaac	500
atggggaaga ggatgtgatt tatacctgga aggccctggg gcaagcagcc	550
aatgagtgcc ataattgggtc catcctcccc atctcctgga gatggggaga	600
aagtgatatg accttcattc gcgttgccag gaaccctgtc agcagaaact	650
tctcaagccc catccttgcc aggaagctct gtgaaggtgc tgctgatgac	700
ccagattcct ccatggtcct cctgtgtctc ctggttggtgc ccctcctgct	750
cagtctcttt gtactggggc tatttctttg gtttctgaag agagagagac	800
aagaagagta cattgaagag aagaagagag tggacatttg tcgggaaact	850
cctaacatat gccccattc tggagagaac acagagtacg acacaatccc	900
tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact	950
ccactgtgga aataccgaaa aagatggaaa atccccactc actgctcacg	1000
atgccagaca caccaaggct atttgccatg gagaatgtta tctagacagc	1050
agtgcaactcc cctaagtctc tgctca	1076

<210> SEQ ID NO 46

<211> LENGTH: 335

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 46

Met Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp	
1 5 10 15	
Gln Leu Thr Gly Ser Ala Ala Ser Gly Pro Val Lys Glu Leu Val	
20 25 30	
Gly Ser Val Gly Gly Ala Val Thr Phe Pro Leu Lys Ser Lys Val	
35 40 45	
Lys Gln Val Asp Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu	
50 55 60	
Val Thr Ile Gln Pro Glu Gly Gly Thr Ile Ile Val Thr Gln Asn	
65 70 75	
Arg Asn Arg Glu Arg Val Asp Phe Pro Asp Gly Gly Tyr Ser Leu	
80 85 90	
Lys Leu Ser Lys Leu Lys Lys Asn Asp Ser Gly Ile Tyr Tyr Val	
95 100 105	
Gly Ile Tyr Ser Ser Ser Leu Gln Gln Pro Ser Thr Gln Glu Tyr	
110 115 120	
Val Leu His Val Tyr Glu His Leu Ser Lys Pro Lys Val Thr Met	
125 130 135	
Gly Leu Gln Ser Asn Lys Asn Gly Thr Cys Val Thr Asn Leu Thr	
140 145 150	
Cys Cys Met Glu His Gly Glu Glu Asp Val Ile Tyr Thr Trp Lys	
155 160 165	
Ala Leu Gly Gln Ala Ala Asn Glu Ser His Asn Gly Ser Ile Leu	
170 175 180	
Pro Ile Ser Trp Arg Trp Gly Glu Ser Asp Met Thr Phe Ile Cys	
185 190 195	

-continued

Val	Ala	Arg	Asn	Pro	Val	Ser	Arg	Asn	Phe	Ser	Ser	Pro	Ile	Leu
			200						205					210
Ala	Arg	Lys	Leu	Cys	Glu	Gly	Ala	Ala	Asp	Asp	Pro	Asp	Ser	Ser
			215						220					225
Met	Val	Leu	Leu	Cys	Leu	Leu	Leu	Val	Pro	Leu	Leu	Leu	Ser	Leu
			230						235					240
Phe	Val	Leu	Gly	Leu	Phe	Leu	Trp	Phe	Leu	Lys	Arg	Glu	Arg	Gln
			245						250					255
Glu	Glu	Tyr	Ile	Glu	Glu	Lys	Lys	Arg	Val	Asp	Ile	Cys	Arg	Glu
			260						265					270
Thr	Pro	Asn	Ile	Cys	Pro	His	Ser	Gly	Glu	Asn	Thr	Glu	Tyr	Asp
			275						280					285
Thr	Ile	Pro	His	Thr	Asn	Arg	Thr	Ile	Leu	Lys	Glu	Asp	Pro	Ala
			290						295					300
Asn	Thr	Val	Tyr	Ser	Thr	Val	Glu	Ile	Pro	Lys	Lys	Met	Glu	Asn
			305						310					315
Pro	His	Ser	Leu	Leu	Thr	Met	Pro	Asp	Thr	Pro	Arg	Leu	Phe	Ala
			320						325					330
Tyr	Glu	Asn	Val	Ile										
			335											

<210> SEQ ID NO 47

<211> LENGTH: 766

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 47

ggctcgagcg tttctgagcc aggggtgacc atgacctgct gcgaaggatg	50
gacatcctgc aatggattca gcctgctggt tctactgctg ttaggagtag	100
ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaattt	150
tctcaaaacc ccatctcttg ctttgagtgg tggttcccag gaattatagg	200
agcaggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa	250
aaagagcgtg ctgcaacaac agaactggaa tgtttctttc atcatttttc	300
agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca	350
ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg	400
ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc	450
ttcaacttgc agtggttttt caatgactct tgtgcacctc ctactggttt	500
caataaaccc accagtaacg acaccatggc gagggtgctg agagcatcta	550
gtttccactt cgattctgaa gaaaacaaac ataggcttat ccacttctca	600
gtatttttag gtctattgct tgttggaatt ctggaggtcc tgtttgggct	650
cagtcagata gtcacggtt tccttggctg tctgtgtgga gtctctaagc	700
gaagaagtca aattgtgtag tttaatggga ataaaatgta agtatcagta	750
gtttgaaaaa aaaaaa	766

<210> SEQ ID NO 48

<211> LENGTH: 229

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 48

Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu

-continued

1	5	10	15
Leu Val Leu Leu Leu	Leu Gly Val Val	Leu Asn Ala Ile Pro	Leu
20		25	30
Ile Val Ser Leu Val	Glu Glu Asp Gln	Phe Ser Gln Asn Pro	Ile
35		40	45
Ser Cys Phe Glu Trp	Trp Phe Pro Gly	Ile Ile Gly Ala Gly	Leu
50		55	60
Met Ala Ile Pro Ala	Thr Thr Met Ser	Leu Thr Ala Arg Lys	Arg
65		70	75
Ala Cys Cys Asn Asn	Arg Thr Gly Met	Phe Leu Ser Ser Phe	Phe
80		85	90
Ser Val Ile Thr Val	Ile Gly Ala Leu	Tyr Cys Met Leu Ile	Ser
95		100	105
Ile Gln Ala Leu Leu	Lys Gly Pro Leu	Met Cys Asn Ser Pro	Ser
110		115	120
Asn Ser Asn Ala Asn	Cys Glu Phe Ser	Leu Lys Asn Ile Ser	Asp
125		130	135
Ile His Pro Glu Ser	Phe Asn Leu Gln	Trp Phe Phe Asn Asp	Ser
140		145	150
Cys Ala Pro Pro Thr	Gly Phe Asn Lys	Pro Thr Ser Asn Asp	Thr
155		160	165
Met Ala Ser Gly Trp	Arg Ala Ser Ser	Phe His Phe Asp Ser	Glu
170		175	180
Glu Asn Lys His Arg	Leu Ile His Phe	Ser Val Phe Leu Gly	Leu
185		190	195
Leu Leu Val Gly Ile	Leu Glu Val Leu	Phe Gly Leu Ser Gln	Ile
200		205	210
Val Ile Gly Phe Leu	Gly Cys Leu Cys	Gly Val Ser Lys Arg	Arg
215		220	225
Ser Gln Ile Val			

<210> SEQ ID NO 49

<211> LENGTH: 636

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 49

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atcgtttctc tgcgttgcca gctcaggtga gccctcgcca aggtgacctc      50
gcaggacact ggtgaaggag cagtgaggaa cctgcagagt cacacagttg      100
ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc      150
cgccccagtg cctctcccc tgcagccctg ccctcgaac tgtgacatgg      200
agagagtgac cctggccctt ctccactagg caggcctgac tgccttgga      250
gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa      300
aaacctgcag ctgagcggac tgatctgcgg agggctcctg gccattgctg      350
ggatcgcggc agttctgagt ggcaaatgca aatacaagag cagccagaag      400
cagcacagtc ctgtacctga gaaggccatc ccaactcatca ctccaggctc      450
tgccactact tgctgagcac aggactggcc tcaggggatg gcctgaagcc      500
taacactggc ccccgacc tcctcccctg ggaggcctta tcctcaagga      550
aggacttctc tccaagggca ggctgttagg cccctttctg atcaggaggc      600
ttctttatga attaaactcg ccccaaccac ccctca      636

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<210> SEQ ID NO 50
 <211> LENGTH: 89
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 50

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Met Glu Arg Val Thr Leu Ala Leu Leu Leu Leu Ala Gly Leu Thr
  1             5             10             15
Ala Leu Glu Ala Asn Asp Pro Phe Ala Asn Lys Asp Asp Pro Phe
             20             25             30
Tyr Tyr Asp Trp Lys Asn Leu Gln Leu Ser Gly Leu Ile Cys Gly
             35             40             45
Gly Leu Leu Ala Ile Ala Gly Ile Ala Ala Val Leu Ser Gly Lys
             50             55             60
Cys Lys Tyr Lys Ser Ser Gln Lys Gln His Ser Pro Val Pro Glu
             65             70             75
Lys Ala Ile Pro Leu Ile Thr Pro Gly Ser Ala Thr Thr Cys
             80             85

```

<210> SEQ ID NO 51
 <211> LENGTH: 1734
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 51

```

gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca      50
gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg      100
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga      150
agacactctg gagagagagg gggctgggca gagatgaagt tccagggggc      200
cctggcctgc ctctgctg ggcctgcct gggcagtgagg gaggtggcc      250
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt      300
ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg      350
caaagaggcc ggaggggag ctgggtctaa agtcagttag gcccttggcc      400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt      450
ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgctct      500
gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac      550
acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt      600
ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg      650
ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg      700
tccacggata ccccgaaaac tcagcaggca gctttggaat gaatcctcag      750
ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac      800
caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca      850
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctgaggtgga      900
ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg      950
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca     1000
gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc     1050
agtggtgga gacagtggaa cagtgggtggc agcagaggtg acagcggcag     1100

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tgagtcctcc tggggatcca gcaccggctc ctctccggc aaccacggtg	1150
ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat	1200
gaagcccgcg ggagcgggga atctgggatt cagggcttca gaggacaggg	1250
agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg	1300
gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga	1350
ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc	1400
tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg	1450
gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcatc	1500
ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact	1550
ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg	1600
aaataaacct tagctgcccc acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa	1734

<210> SEQ ID NO 52

<211> LENGTH: 440

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 52

Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys	
1 5 10 15	
Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser	
20 25 30	
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp	
35 40 45	
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly	
50 55 60	
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr	
65 70 75	
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly	
80 85 90	
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala	
95 100 105	
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val	
110 115 120	
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val	
125 130 135	
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile	
140 145 150	
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro	
155 160 165	
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser	
170 175 180	
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln	
185 190 195	
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly	
200 205 210	
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln	
215 220 225	

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Asn	Glu	Gly	Cys	Thr	Asn	Pro	Pro	Pro	Ser	Gly	Ser	Gly	Gly	Gly	230	235	240
Ser	Ser	Asn	Ser	Gly	Gly	Gly	Ser	Gly	Ser	Gln	Ser	Gly	Ser	Ser	245	250	255
Gly	Ser	Gly	Ser	Asn	Gly	Asp	Asn	Asn	Asn	Gly	Ser	Ser	Ser	Gly	260	265	270
Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser	275	280	285
Ser	Gly	Gly	Ser	Ser	Gly	Gly	Ser	Ser	Gly	Asn	Ser	Gly	Gly	Ser	290	295	300
Arg	Gly	Asp	Ser	Gly	Ser	Glu	Ser	Ser	Trp	Gly	Ser	Ser	Thr	Gly	305	310	315
Ser	Ser	Ser	Gly	Asn	His	Gly	Gly	Ser	Gly	Gly	Gly	Asn	Gly	His	320	325	330
Lys	Pro	Gly	Cys	Glu	Lys	Pro	Gly	Asn	Glu	Ala	Arg	Gly	Ser	Gly	335	340	345
Glu	Ser	Gly	Ile	Gln	Gly	Phe	Arg	Gly	Gln	Gly	Val	Ser	Ser	Asn	350	355	360
Met	Arg	Glu	Ile	Ser	Lys	Glu	Gly	Asn	Arg	Leu	Leu	Gly	Gly	Ser	365	370	375
Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly	380	385	390
Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser	395	400	405
Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser	410	415	420
Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg	425	430	435
Ser	Ser	Arg	Ile	Pro											440		

<210> SEQ ID NO 53

<211> LENGTH: 1676

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 53

ggagaagagg ttgtgtggga caagctgctc cgcacagaag gatgtcgctg	50
ctgagcctgc cctggctggg cctcagaccg gtggcaatgt ccccatggct	100
actcctgctg ctggttgtgg gctcctggct actcgcccgc atcctggctt	150
ggacctatgc cttctataac aactgccgcc ggctccagtg tttccacag	200
ccccaaaac ggaactggtt ttgggggtcac ctgggcctga tcaactctac	250
agaggagggc ttgaaggact cgacccagat gtcggccacc tattcccagg	300
gctttacggt atggctgggt cccatcatcc ccttcacgtg tttatgccac	350
cctgacacca tccggtctat caccaatgcc tcagctgcca ttgcacccaa	400
ggataatctc ttcacaggt tcctgaagcc ctggctggga gaagggatac	450
tgctgagtgg cggtgacaag tggagccgcc accgtcggat gctgacgcc	500
gccttcatt tcaacatcct gaagtctat ataacgatct tcaacaagag	550
tgcaaacatc atgcttgaca agtggcagca cctggcctca gagggcagca	600
gtcgtctgga catgtttgag cacatcagcc tcatgacctt ggacagtcta	650

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cagaaatgca tcttcagctt tgacagccat tgtcaggaga ggcccagtga	700
atatattgcc accatcttgg agctcagtgc ccttgtagag aaaagaagcc	750
agcatatcct ccagcacatg gactttctgt attacctctc ccatgacggg	800
cggcgcttcc acagggcctg ccgcctggtg catgacttca cagacgctgt	850
catccgggag cggcgtcgca ccctccccac tcagggtatt gatgattttt	900
tcaaagacaa agccaagtcc aagactttgg atttcattga tgtgcttctg	950
ctgagcaagg atgaagatgg gaaggcattg tcagatgagg atataagagc	1000
agaggctgac accttcatgt ttggaggcca tgacaccacg gccagtggcc	1050
tctcctgggt cctgtacaac cttgcgaggc acccagaata ccaggagcgc	1100
tgccgacagg aggtgcaaga gcttctgaag gaccgcgac ctaaagagat	1150
tgaatgggac gacctggccc agctgccctt cctgaccatg tgcgtgaagg	1200
agagcctgag gttacatccc ccagctccct tcatctcccg atgctgcacc	1250
caggacattg ttctcccaga tggccgagtc atccccaag gcattacctg	1300
cctcatcgat attatagggg tccatcacia cccaactgtg tggccgagtc	1350
ctgaggtcta cgacccttc cgctttgacc cagagaacag caaggggagg	1400
tcacctctgg cttttattcc ttctccgca gggcccagga actgcatcgg	1450
gcaggcggtc gccatggcgg agatgaaagt ggtcctggcg ttgatgctgc	1500
tgcaattccg gttcctgcca gaccacactg agccccgag gaagctggaa	1550
ttgatcatgc gcgccgaggg cgggctttgg ctgcgggtgg agccccgaa	1600
tgtaggcttg cagtgacttt ctgacccatc cacctgtttt tttgcagatt	1650
gtcatgaata aaacggtgct gtcaaaa	1676

<210> SEQ ID NO 54

<211> LENGTH: 524

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 54

Met Ser Leu Leu Ser Leu Pro Trp Leu Gly Leu Arg Pro Val Ala	
1 5 10 15	
Met Ser Pro Trp Leu Leu Leu Leu Val Val Gly Ser Trp Leu	
20 25 30	
Leu Ala Arg Ile Leu Ala Trp Thr Tyr Ala Phe Tyr Asn Asn Cys	
35 40 45	
Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe	
50 55 60	
Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys	
65 70 75	
Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val	
80 85 90	
Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp	
95 100 105	
Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys	
110 115 120	
Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly	
125 130 135	
Ile Leu Leu Ser Gly Gly Asp Lys Trp Ser Arg His Arg Arg Met	
140 145 150	

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Leu Thr Pro Ala Phe His Phe Asn Ile	Leu Lys Ser Tyr Ile Thr
155	160 165
Ile Phe Asn Lys Ser Ala Asn Ile Met	Leu Asp Lys Trp Gln His
170	175 180
Leu Ala Ser Glu Gly Ser Ser Arg Leu	Asp Met Phe Glu His Ile
185	190 195
Ser Leu Met Thr Leu Asp Ser Leu Gln	Lys Cys Ile Phe Ser Phe
200	205 210
Asp Ser His Cys Gln Glu Arg Pro Ser	Glu Tyr Ile Ala Thr Ile
215	220 225
Leu Glu Leu Ser Ala Leu Val Glu Lys	Arg Ser Gln His Ile Leu
230	235 240
Gln His Met Asp Phe Leu Tyr Tyr Leu	Ser His Asp Gly Arg Arg
245	250 255
Phe His Arg Ala Cys Arg Leu Val His	Asp Phe Thr Asp Ala Val
260	265 270
Ile Arg Glu Arg Arg Arg Thr Leu Pro	Thr Gln Gly Ile Asp Asp
275	280 285
Phe Phe Lys Asp Lys Ala Lys Ser Lys	Thr Leu Asp Phe Ile Asp
290	295 300
Val Leu Leu Leu Ser Lys Asp Glu Asp	Gly Lys Ala Leu Ser Asp
305	310 315
Glu Asp Ile Arg Ala Glu Ala Asp Thr	Phe Met Phe Gly Gly His
320	325 330
Asp Thr Thr Ala Ser Gly Leu Ser Trp	Val Leu Tyr Asn Leu Ala
335	340 345
Arg His Pro Glu Tyr Gln Glu Arg Cys	Arg Gln Glu Val Gln Glu
350	355 360
Leu Leu Lys Asp Arg Asp Pro Lys Glu	Ile Glu Trp Asp Asp Leu
365	370 375
Ala Gln Leu Pro Phe Leu Thr Met Cys	Val Lys Glu Ser Leu Arg
380	385 390
Leu His Pro Pro Ala Pro Phe Ile Ser	Arg Cys Cys Thr Gln Asp
395	400 405
Ile Val Leu Pro Asp Gly Arg Val Ile	Pro Lys Gly Ile Thr Cys
410	415 420
Leu Ile Asp Ile Ile Gly Val His His	Asn Pro Thr Val Trp Pro
425	430 435
Asp Pro Glu Val Tyr Asp Pro Phe Arg	Phe Asp Pro Glu Asn Ser
440	445 450
Lys Gly Arg Ser Pro Leu Ala Phe Ile	Pro Phe Ser Ala Gly Pro
455	460 465
Arg Asn Cys Ile Gly Gln Ala Phe Ala	Met Ala Glu Met Lys Val
470	475 480
Val Leu Ala Leu Met Leu Leu His Phe	Arg Phe Leu Pro Asp His
485	490 495
Thr Glu Pro Arg Arg Lys Leu Glu Leu	Ile Met Arg Ala Glu Gly
500	505 510
Gly Leu Trp Leu Arg Val Glu Pro Leu	Asn Val Gly Leu Gln
515	520

<210> SEQ ID NO 55

<211> LENGTH: 644

-continued

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 55

atcgcatcaa ttgggagtag catcttcctc atgggaccag tgaacacagct	50
gaagcgaatg tttgagccta ctcgtttgat tgcaactatc atggtgctgt	100
tgtgttttgc acttaccctg tgttctgcct tttggtggca taacaaggga	150
cttgcaactta tcttctgcat tttgcagtct ttggcattga cgtggtacag	200
cctttccttc ataccatttg caagggatgc tgtgaagaag tgttttgccg	250
tgtgtcttgc ataattcatg gccagtttta tgaagctttg gaaggcacta	300
tggacagaag ctggtggaca gttttgtaac tatcttcgaa acctctgtct	350
tacagacatg tgccttttat cttgcagcaa tgtgttgctt gtgattcgaa	400
catttgaggg ttacttttgg aagcaacaat acattctcga acctgaatgt	450
cagtagcaca ggatgagaag tgggttctgt atcttgtgga gtggaatctt	500
cctcatgtac ctgtttcctc tctggatgtt gtcccaactga attcccatga	550
atacaaacct attcagcaac agcaaaaaaa aaaaaaaaaa aaaaaaaaaa	600
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa	644

<210> SEQ ID NO 56

<211> LENGTH: 77

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 56

Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg	
1 5 10 15	
Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu	
20 25 30	
Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe	
35 40 45	
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe	
50 55 60	
Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys	
65 70 75	
Leu Ala	

<210> SEQ ID NO 57

<211> LENGTH: 3334

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 57

cggctcgagc tcgagccgaa tcggctcgag gggcagtgga gcaccagca	50
ggccgccaac atgctctgtc tgtgcctgta cgtgccggtc atcggggaag	100
cccagaccga gttccagtac tttgagtcga aggggctccc tgccgagctg	150
aagtccattt tcaagctcag tgtcttcac ccctcccagg aattctccac	200
ctaccgccag tggaagcaga aaattgtaca agctggagat aaggaccttg	250
atgggcagct agactttgaa gaatttgtcc attatctcca agatcatgag	300
aagaagctga ggctggtgtt taagattttg gacaaaaaga atgatggacg	350
cattgacgcg caggagatca tgcagtcctt gcgggacttg ggagtcaaga	400

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tatctgaaca gcaggcagaa aaaattctca agagcatgga taaaaacggc	450
acgatgacca tcgactggaa cgagtggaga gactaccacc tcctccaccc	500
cgtggaaaac atccccgaga tcattcctcta ctggaagcat tccacgatct	550
ttgatgtggg tgagaatcta acggtcccgg atgagttcac agtggaggag	600
aggcagacgg ggatgtggg gagacacctg gtggcaggag gtggggcagg	650
ggcgtatcc agaacctgca cggccccctt ggacaggctc aaggtgctca	700
tgcaggtcca tgccctccgc agcaacaaca tgggcatcgt tggtggttc	750
actcagatga ttcgagaagg aggggccagg tcaactctggc ggggcaatgg	800
catcaacgct ctcaaaattg cccccgaatc agccatcaa tcatggcct	850
atgagcagat caagcgcctt gttggtagtg accaggagac tctgaggatt	900
cacgagaggc ttgtggcagg gtccttgga ggggccatcg ccagagcag	950
catctacca atggagggtcc tgaagaccgg gatggcgctg cggaagacag	1000
gccagtactc aggaatgctg gactgcgcca ggaggatcct gccagagag	1050
ggggtggccg ccttctacaa aggctatgtc cccaacatgc tgggcatcat	1100
ccctatgcc ggcatcgacc ttgcagtcta cgagacgctc aagaatgcct	1150
ggctgcagca ctatgcagtg aacagcgcgg accccggcgt gtttgtgctc	1200
ctggcctgtg gcaccatgtc cagtacctgt gccagctgg ccagctaccc	1250
cctggcccta gtcaggaccc ggatgcaggc gcaagcctct attgaggcg	1300
ctccggagggt gacctgagc agcctcttca aacatatcct gcggaccgag	1350
ggggccttcg ggctgtacag ggggctggcc cccaacttca tgaaggtcat	1400
cccagctgtg agcatcagct acgtggtcta cgagaacctg aagatcacc	1450
tgggcgtgca gtcgcggtga cggggggagg gccgccggc agtggactcg	1500
ctgatcctgg gccgcagcct ggggtgtgca gccatctcat tctgtgaatg	1550
tgccaacact aagctgtctc gagccaagct gtgaaaacc tagacgcacc	1600
cgcagggagg gtggggagag ctggcaggcc cagggttgt cctgctgacc	1650
ccagcagacc ctctgttggt ttccagcgaa gaccacaggc attccttagg	1700
gtccagggtc agcaggctcc gggctcacat gtgtaaggac aggacathtt	1750
ctgcagtgcc tgccaatagt gagcttgag cctggaggcc ggcttagttc	1800
ttccatttca cccttgacg cagctgttg gacggcccc tgccctctgg	1850
tctgccgtgc atctccctgt gccctcttgc tgccctgcctg tctgctgagg	1900
taaggtggga ggagggtac agcccacatc ccaccccctc gtccaatccc	1950
ataatccatg atgaaagggt aggtcacgtg gcctcccagg cctgacttcc	2000
caacctacag cattgacgcc aacttggtgtg tgaagggaaga ggaaaggatc	2050
tggccttgtg gtcactggca tctgagccct gctgatggct ggggctctcg	2100
ggcatgcttg ggagtgcagg gggctcgggc tgccctggcct ggctgcacag	2150
aaggcaagtg ctggggctca tgggtgcttg agctggcctg gacctgtca	2200
ggatggggcc caccctcagaa ccaaactcac tgtccccact gtggcatgag	2250
ggcagtggag caccatgttt gagggcgaag ggcagagcgt ttgtgtgttc	2300
tggggaggga aggaaaagggt gttggaggcc ttaattatgg actgttgga	2350

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aaaggggtttt gtccagaagg acaagccgga caaatgagcg acttctgtgc	2400
ttccagagga agacgaggga gcaggagctt ggctgactgc tcagagtctg	2450
ttctgacgcc ctgggggttc ctgtccaacc ccagcagggg cgcagcggga	2500
ccagcccccac attccacttg tgtcactgct tggaacctat ttattttgta	2550
tttatttgaa cagagttagt tcctaactat ttttatagat ttgtttaatt	2600
aatagcttgt cattttcaag ttcatttttt attcatattt atgttcatgg	2650
ttgattgtac cttcccaagc ccgcccagtg ggatgggagg aggaggagaa	2700
ggggggcctt gggccgctgc agtcacatct gtccagagaa attccttttg	2750
ggactggagg cagaaaagcg gccagaaggc agcagccctg gctcctttcc	2800
tttggcaggt tggggaaggg ctgtcccccga gccttaggat ttcagggttt	2850
gactgggggc gtggagagag agggaggaac ctcaataacc ttgaaggtgg	2900
aatccagtta tttcctgcgc tgcgagggtt tctttatttc actcttttct	2950
gaatgtcaag gcagtgaggt gcctctcact gtgaatttgt ggtgggagg	3000
ggctggagga gaggggtggg ggctggctcc gtccctccca gccttctgct	3050
gcccttgctt aacaatgccg gccaaactggc gacctcacgg ttgcacttcc	3100
attccaccag aatgacctga tgaggaaatc ttcaatagga tgcaaagatc	3150
aatgcaaaaa ttgttatata tgaacatata actggagtcg tcaaaaagca	3200
aattaagaaa gaattggacg ttagaagttg tcatttaaag cagccttcta	3250
ataaagttgt ttcaaagctg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	3300
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa	3334

<210> SEQ ID NO 58

<211> LENGTH: 469

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 58

Met	Leu	Cys	Leu	Cys	Leu	Tyr	Val	Pro	Val	Ile	Gly	Glu	Ala	Gln
1				5					10					15
Thr	Glu	Phe	Gln	Tyr	Phe	Glu	Ser	Lys	Gly	Leu	Pro	Ala	Glu	Leu
			20						25					30
Lys	Ser	Ile	Phe	Lys	Leu	Ser	Val	Phe	Ile	Pro	Ser	Gln	Glu	Phe
			35						40					45
Ser	Thr	Tyr	Arg	Gln	Trp	Lys	Gln	Lys	Ile	Val	Gln	Ala	Gly	Asp
			50						55					60
Lys	Asp	Leu	Asp	Gly	Gln	Leu	Asp	Phe	Glu	Glu	Phe	Val	His	Tyr
			65						70					75
Leu	Gln	Asp	His	Glu	Lys	Lys	Leu	Arg	Leu	Val	Phe	Lys	Ile	Leu
			80						85					90
Asp	Lys	Lys	Asn	Asp	Gly	Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln
			95						100					105
Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu
			110						115					120
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp
			125						130					135
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn
			140						145					150
Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp

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155	160	165
Val Gly Glu Asn Leu Thr Val Pro Asp	Glu Phe Thr Val Glu Glu	
170	175	180
Arg Gln Thr Gly Met Trp Trp Arg His	Leu Val Ala Gly Gly Gly	
185	190	195
Ala Gly Ala Val Ser Arg Thr Cys Thr	Ala Pro Leu Asp Arg Leu	
200	205	210
Lys Val Leu Met Gln Val His Ala Ser	Arg Ser Asn Asn Met Gly	
215	220	225
Ile Val Gly Gly Phe Thr Gln Met Ile	Arg Glu Gly Gly Ala Arg	
230	235	240
Ser Leu Trp Arg Gly Asn Gly Ile Asn	Val Leu Lys Ile Ala Pro	
245	250	255
Glu Ser Ala Ile Lys Phe Met Ala Tyr	Glu Gln Ile Lys Arg Leu	
260	265	270
Val Gly Ser Asp Gln Glu Thr Leu Arg	Ile His Glu Arg Leu Val	
275	280	285
Ala Gly Ser Leu Ala Gly Ala Ile Ala	Gln Ser Ser Ile Tyr Pro	
290	295	300
Met Glu Val Leu Lys Thr Arg Met Ala	Leu Arg Lys Thr Gly Gln	
305	310	315
Tyr Ser Gly Met Leu Asp Cys Ala Arg	Arg Ile Leu Ala Arg Glu	
320	325	330
Gly Val Ala Ala Phe Tyr Lys Gly Tyr	Val Pro Asn Met Leu Gly	
335	340	345
Ile Ile Pro Tyr Ala Gly Ile Asp Leu	Ala Val Tyr Glu Thr Leu	
350	355	360
Lys Asn Ala Trp Leu Gln His Tyr Ala	Val Asn Ser Ala Asp Pro	
365	370	375
Gly Val Phe Val Leu Leu Ala Cys Gly	Thr Met Ser Ser Thr Cys	
380	385	390
Gly Gln Leu Ala Ser Tyr Pro Leu Ala	Leu Val Arg Thr Arg Met	
395	400	405
Gln Ala Gln Ala Ser Ile Glu Gly Ala	Pro Glu Val Thr Met Ser	
410	415	420
Ser Leu Phe Lys His Ile Leu Arg Thr	Glu Gly Ala Phe Gly Leu	
425	430	435
Tyr Arg Gly Leu Ala Pro Asn Phe Met	Lys Val Ile Pro Ala Val	
440	445	450
Ser Ile Ser Tyr Val Val Tyr Glu Asn	Leu Lys Ile Thr Leu Gly	
455	460	465

Val Gln Ser Arg

<210> SEQ ID NO 59

<211> LENGTH: 1658

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 59

ggaaggcagc ggcagctcca ctcagccagt acccagatac gctgggaacc	50
ttccccagcc atggcttccc tggggcagat cctcttctgg agcataatta	100
gcatcatcat tattctggct ggagcaattg cactcatcat tggctttggt	150
atttcaggga gacactccat cacagtcact actgtcgcct cagctgggaa	200

-continued

cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac	250
tttctgatat cgtgatacaa tggtgaagg aaggtgtttt aggttggtc	300
catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt	350
cagaggcccg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct	400
ctttgcggct gaaaaacgtg caactcacag atgctggcac ctacaaatgt	450
tatatcatca cttctaaagg caaggggaat gctaaccttg agtataaac	500
tggagccttc agcatgccg aagtgaatgt ggactataat gccagctcag	550
agaccttgct gtgtgaggct ccccgatggt tccccagcc cacagtggtc	600
tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac	650
cagctttgag ctgaactctg agaatgtgac catgaaggtt gtgtctgtgc	700
tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac	750
attgccaaag caacagggga tatcaaagt acagaatcgg agatcaaaag	800
gcggagtccac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt	850
ctttctttgc catcagctgg gcacttctgc ctctcagccc ttacctgatg	900
ctaaaataat gtgccttgcc cacaaaaaag catgcaaagt cattgttaca	950
acagggatct acagaactat ttcaccacca gatatgacct agttttatat	1000
ttctgggagg aaatgaattc atatctagaa gtctggagt agcaacaag	1050
agcaagaac aaaaagaagc caaaagcaga aggtccaat atgaacaaga	1100
taaatctatc ttcaaagaca tattagaagt tgggaaaata attcatgtga	1150
actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt	1200
gcatccccag atctcaggga cctccccctg cctgtcacct ggggagtga	1250
aggacaggat agtgcatgtt ctttgtctct gaatttttag ttatatgtgc	1300
tgtaatgttg ctctgaggaa gccctggaa agtctatccc aacatatcca	1350
catcttatat tccacaaatt aagctgtagt atgtacccta agacgtgct	1400
aattgactgc cacttcgcaa ctacgggag gctgcatttt agtaatgggt	1450
caaatgattc actttttatg atgcttcaa aggtgccttg gcttctcttc	1500
ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa	1550
acagagcagt cggggacacc gatattataa ataaactgag caccttcttt	1600
ttaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	1650
aaaaaaaa	1658

<210> SEQ ID NO 60

<211> LENGTH: 282

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 60

Met	Ala	Ser	Leu	Gly	Gln	Ile	Leu	Phe	Trp	Ser	Ile	Ile	Ser	Ile
1				5					10					15

Ile	Ile	Ile	Leu	Ala	Gly	Ala	Ile	Ala	Leu	Ile	Ile	Gly	Phe	Gly
			20						25					30

Ile	Ser	Gly	Arg	His	Ser	Ile	Thr	Val	Thr	Thr	Val	Ala	Ser	Ala
			35						40					45

Gly	Asn	Ile	Gly	Glu	Asp	Gly	Ile	Leu	Ser	Cys	Thr	Phe	Glu	Pro

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50	55	60
Asp Ile Lys Leu Ser	Asp Ile Val Ile Gln Trp Leu Lys Glu Gly	
65	70	75
Val Leu Gly Leu Val	His Glu Phe Lys Glu Gly Lys Asp Glu Leu	
80	85	90
Ser Glu Gln Asp Glu	Met Phe Arg Gly Arg Thr Ala Val Phe Ala	
95	100	105
Asp Gln Val Ile Val	Gly Asn Ala Ser Leu Arg Leu Lys Asn Val	
110	115	120
Gln Leu Thr Asp Ala	Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser	
125	130	135
Lys Gly Lys Gly Asn	Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe	
140	145	150
Ser Met Pro Glu Val	Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr	
155	160	165
Leu Arg Cys Glu Ala	Pro Arg Trp Phe Pro Gln Pro Thr Val Val	
170	175	180
Trp Ala Ser Gln Val	Asp Gln Gly Ala Asn Phe Ser Glu Val Ser	
185	190	195
Asn Thr Ser Phe Glu	Leu Asn Ser Glu Asn Val Thr Met Lys Val	
200	205	210
Val Ser Val Leu Tyr	Asn Val Thr Ile Asn Asn Thr Tyr Ser Cys	
215	220	225
Met Ile Glu Asn Asp	Ile Ala Lys Ala Thr Gly Asp Ile Lys Val	
230	235	240
Thr Glu Ser Glu Ile	Lys Arg Arg Ser His Leu Gln Leu Leu Asn	
245	250	255
Ser Lys Ala Ser Leu	Cys Val Ser Ser Phe Phe Ala Ile Ser Trp	
260	265	270
Ala Leu Leu Pro Leu	Ser Pro Tyr Leu Met Leu Lys	
275	280	

<210> SEQ ID NO 61

<211> LENGTH: 1617

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 61

tgacgtcaga atcaccatgg ccagctatcc ttaccggcag ggctgccag	50
gagctgcagg acaagcacca ggagcccctc cgggtagcta ctaccctgga	100
cccccaata gtggagggca gtatggtagt gggctacccc ctggtggtgg	150
ttatgggggt cctgcccctg gagggcctta tggaccacca gctggtggag	200
ggccttatgg acacccaat cctgggatgt tcccctctgg aactccagga	250
ggaccatatg gcggtgcagc tcccgggggc ccctatggtc agccacctcc	300
aagttcctac ggtgcccagc agcctgggct ttatggacag ggtggcgccc	350
ctcccaatgt ggatcctgag gcctactcct ggttccagtc ggtggactca	400
gatcacagtg gctatatctc catgaaggag ctaaagcagg ccctgggtcaa	450
ctgcaattgg tcttcattca atgatgagac ctgcctcatg atgataaaca	500
tgtttgacaa gaccaagtca ggccgcatcg atgtctacgg cttctcagcc	550
ctgtggaaat tcatccagca gtggaagaac ctcttccagc agtatgaccg	600

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ggaccgctcg ggctccatta gctacacaga gctgcagcaa gctctgtccc      650
aaatgggcta caacctgagc cccaggttca cccagcttct ggtctccgc       700
tactgccac gctctgccaa tcctgccatg cagcttgacc gcttcacca       750
ggtgtgcacc cagctgcagg tgctgacaga ggccttccgg gagaaggaca      800
cagctgtaca aggcaacatc cggctcagct tcgaggactt cgtcaccatg      850
acagcttctc ggatgctatg acccaacat ctgtggagag tggagtgcac      900
caggggacctt tcctggcttc ttagagttag agaagtatgt ggacatctct     950
tcttttctcg tccctctaga agaacattct cccttgcttg atgcaacact     1000
gttccaaaag aggggtggaga gtccctgcac atagccacca aatagtgagg     1050
accggggctg aggccacaca gatagggggc tgatggagga gaggatagaa     1100
gttgaatgtc ctgatggcca tgagcagttg agtggcacag cctggcacca     1150
ggagcaggtc cttgtaatgg agttagtgtc cagtcagctg agtccacccc     1200
tgatgccagt ggtgagtgtt catcggcctg ttaccgtagg tacctgtgtt     1250
ccctcaccag gccatcctgt caaacgagcc cattttctcc aaagtggaaat     1300
ctgaccaagc atgagagaga tctgtctatg ggaccagtgg cttggattct     1350
gccacaccca taaatccttg tgtgttaact tctagctgcc tggggctggc     1400
cctgctcaga caaatctgct ccctgggcat ctttggccag gcttctgccc     1450
cctgcagctg ggaccctca cttgcctgcc atgctctgct cggcttcagt     1500
ctccaggaga cagtggtcac ctctccctgc caatactttt ttttaattgc     1550
attttttttc atttggggcc aaaagtccag tgaaattgta agcttcaata     1600
aaaggatgaa actctga                                           1617

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<210> SEQ ID NO 62

<211> LENGTH: 284

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 62

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Met Ala Ser Tyr Pro Tyr Arg Gln Gly Cys Pro Gly Ala Ala Gly
  1             5             10             15
Gln Ala Pro Gly Ala Pro Pro Gly Ser Tyr Tyr Pro Gly Pro Pro
          20             25             30
Asn Ser Gly Gly Gln Tyr Gly Ser Gly Leu Pro Pro Gly Gly Gly
          35             40             45
Tyr Gly Gly Pro Ala Pro Gly Gly Pro Tyr Gly Pro Pro Ala Gly
          50             55             60
Gly Gly Pro Tyr Gly His Pro Asn Pro Gly Met Phe Pro Ser Gly
          65             70             75
Thr Pro Gly Gly Pro Tyr Gly Gly Ala Ala Pro Gly Gly Pro Tyr
          80             85             90
Gly Gln Pro Pro Pro Ser Ser Tyr Gly Ala Gln Gln Pro Gly Leu
          95             100            105
Tyr Gly Gln Gly Gly Ala Pro Pro Asn Val Asp Pro Glu Ala Tyr
          110            115            120
Ser Trp Phe Gln Ser Val Asp Ser Asp His Ser Gly Tyr Ile Ser
          125            130            135
Met Lys Glu Leu Lys Gln Ala Leu Val Asn Cys Asn Trp Ser Ser
          140            145            150

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Phe Asn Asp Glu Thr Cys Leu Met Met	Ile Asn Met Phe Asp Lys
155	160 165
Thr Lys Ser Gly Arg Ile Asp Val Tyr	Gly Phe Ser Ala Leu Trp
170	175 180
Lys Phe Ile Gln Gln Trp Lys Asn Leu	Phe Gln Gln Tyr Asp Arg
185	190 195
Asp Arg Ser Gly Ser Ile Ser Tyr Thr	Glu Leu Gln Gln Ala Leu
200	205 210
Ser Gln Met Gly Tyr Asn Leu Ser Pro	Gln Phe Thr Gln Leu Leu
215	220 225
Val Ser Arg Tyr Cys Pro Arg Ser Ala	Asn Pro Ala Met Gln Leu
230	235 240
Asp Arg Phe Ile Gln Val Cys Thr Gln	Leu Gln Val Leu Thr Glu
245	250 255
Ala Phe Arg Glu Lys Asp Thr Ala Val	Gln Gly Asn Ile Arg Leu
260	265 270
Ser Phe Glu Asp Phe Val Thr Met Thr	Ala Ser Arg Met Leu
275	280

<210> SEQ ID NO 63

<211> LENGTH: 1234

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 63

caggatgcag ggccgcgtgg cagggagctg cgctcctctg ggcctgctcc	50
tggtctgtct tcatctccca ggcctctttg cccggagcat cgggtgtgtg	100
gaggagaaag ttccccaaa cttcgggacc aacttgctc agctcggaca	150
accttctctc actggcccct ctaactctga acatccgcag cccgctctgg	200
accctaggtc taatgacttg gcaagggttc ctctgaagct cagcgtgcct	250
ccatcagatg gcttcccacc tgcaggaggt tctgcagtgc agagggtggc	300
tccactgtgg gggctgctg ccatggattc ctggccccct gaggatcctt	350
ggcagatgat ggctgctgcg gctgaggacc gcctggggga agcgtgcct	400
gaagaactct cttacctctc cagtgtctcg gccctcgtc cgggcagtgg	450
ccctttgctt ggggagtctt ctcccgatgc cacaggcctc tcacctgagg	500
cttcactcct ccaccaggac tcggagtcca gacgactgcc ccgttcta	550
tcactgggag ccgggggaaa aatcctttcc caacgcctc cctggtctct	600
catccacagg gttctgcctg atcacccctg gggtagcctg aatcccagtg	650
tgctctgggg aggtggaggc cctgggactg gttggggaac gaggccatg	700
ccacaccctg agggaatctg gggtagcaat aatcaacccc caggtaccag	750
ctggggaaat attaatcggg atccaggagg cagctgggga aatattaatc	800
ggtagccagg aggcagctgg gggaatatta atcggtatcc aggaggcagc	850
tgggggaata ttcatctata cccaggatcc aataacccat ttcctcctgg	900
agttctccgc cctcctggct cttcttgtaa catcccagct ggcttcccta	950
atcctccaag ccctagggtg cagtggggct agagcacgat agagggaac	1000
ccaacattgg gagtttaggt cctgtcccg ccccttctg tgtgggctca	1050
atccaggccc tgtaaacatg ttccagcac tatccccact tttcagtgcc	1100

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ttccctgctc atctccaata aaataaaagc acttatgaaa aaaaaaaaaa 1150

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

<210> SEQ ID NO 64

<211> LENGTH: 325

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 64

Met Gln Gly Arg Val Ala Gly Ser Cys Ala Pro Leu Gly Leu Leu
1 5 10 15

Leu Val Cys Leu His Leu Pro Gly Leu Phe Ala Arg Ser Ile Gly
20 25 30

Val Val Glu Glu Lys Val Ser Gln Asn Phe Gly Thr Asn Leu Pro
35 40 45

Gln Leu Gly Gln Pro Ser Ser Thr Gly Pro Ser Asn Ser Glu His
50 55 60

Pro Gln Pro Ala Leu Asp Pro Arg Ser Asn Asp Leu Ala Arg Val
65 70 75

Pro Leu Lys Leu Ser Val Pro Pro Ser Asp Gly Phe Pro Pro Ala
80 85 90

Gly Gly Ser Ala Val Gln Arg Trp Pro Pro Ser Trp Gly Leu Pro
95 100 105

Ala Met Asp Ser Trp Pro Pro Glu Asp Pro Trp Gln Met Met Ala
110 115 120

Ala Ala Ala Glu Asp Arg Leu Gly Glu Ala Leu Pro Glu Glu Leu
125 130 135

Ser Tyr Leu Ser Ser Ala Ala Ala Leu Ala Pro Gly Ser Gly Pro
140 145 150

Leu Pro Gly Glu Ser Ser Pro Asp Ala Thr Gly Leu Ser Pro Glu
155 160 165

Ala Ser Leu Leu His Gln Asp Ser Glu Ser Arg Arg Leu Pro Arg
170 175 180

Ser Asn Ser Leu Gly Ala Gly Gly Lys Ile Leu Ser Gln Arg Pro
185 190 195

Pro Trp Ser Leu Ile His Arg Val Leu Pro Asp His Pro Trp Gly
200 205 210

Thr Leu Asn Pro Ser Val Ser Trp Gly Gly Gly Gly Pro Gly Thr
215 220 225

Gly Trp Gly Thr Arg Pro Met Pro His Pro Glu Gly Ile Trp Gly
230 235 240

Ile Asn Asn Gln Pro Pro Gly Thr Ser Trp Gly Asn Ile Asn Arg
245 250 255

Tyr Pro Gly Gly Ser Trp Gly Asn Ile Asn Arg Tyr Pro Gly Gly
260 265 270

Ser Trp Gly Asn Ile Asn Arg Tyr Pro Gly Gly Ser Trp Gly Asn
275 280 285

Ile His Leu Tyr Pro Gly Ile Asn Asn Pro Phe Pro Pro Gly Val
290 295 300

Leu Arg Pro Pro Gly Ser Ser Trp Asn Ile Pro Ala Gly Phe Pro
305 310 315

Asn Pro Pro Ser Pro Arg Leu Gln Trp Gly

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320	325	
<210> SEQ ID NO 65		
<211> LENGTH: 422		
<212> TYPE: DNA		
<213> ORGANISM: Homo Sapien		
<400> SEQUENCE: 65		
aaggagaggc caccgggact tcaagtgtctc ctccatccca ggagcgcagt		50
ggccactatg gggctctgggc tgccccttgt cctcctcttg accctccttg		100
gcagctcaca tggaacaggc cggggtatga ctttgcaact gaagctgaag		150
gagtcttttc tgacaaatc ctcctatgag tccagcttcc tggaattgct		200
tgaaaagctc tgccctctcc tccatctccc ttcaggggacc agcgtcaccc		250
tccacatgc aagatctcaa cccatgttg tctgcaacac atgacagcca		300
ttgaagcctg tgccttctt ggcccgggct tttgggcccgg ggatgcagga		350
ggcaggcccc gaccctgtct ttcagcaggc cccaccctc ctgagtggca		400
ataaataaaa ttcggtatgc tg		422

<210> SEQ ID NO 66		
<211> LENGTH: 78		
<212> TYPE: PRT		
<213> ORGANISM: Homo Sapien		
<400> SEQUENCE: 66		
Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly		
1 5 10 15		
Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu		
20 25 30		
Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu		
35 40 45		
Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly		
50 55 60		
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val		
65 70 75		
Cys Asn Thr		

<210> SEQ ID NO 67		
<211> LENGTH: 744		
<212> TYPE: DNA		
<213> ORGANISM: Homo Sapien		
<400> SEQUENCE: 67		
acggaccgag ggttcgaggg agggacacgg accaggaacc tgagctagggt		50
caaagacgcc cgggccaggt gcccgcgc aggtgccct gcccgagat		100
gcggtaggag gggcgagcgc gagaagcccc ttcctcggcg ctgccaaacc		150
gccaccacgc ccatggcgaa ccccgggctg gggctgcttc tggcgctggg		200
cctgccgttc ctgctggccc gctggggccg agcctggggg caaatacaga		250
ccacttctgc aaatgagaat agcactgttt tgccttcac caccagctcc		300
agctccgatg gcaacctgcg tccggaagcc atcactgcta tcatcgtggt		350
cttctccctc ttggctgcct tgctcctggc tgtggggctg gcaactgttg		400
tgcggaagct tcgggagaag cggcagacgg agggcaccta ccggcccagt		450

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agcgaggagc agttctccca tgcagccgag gcccgggccc ctcaggactc	500
caaggagacg gtgcagggct gcctgcccat ctaggtcccc tctcctgcat	550
ctgtctccct tcattgctgt gtgaccttgg ggaaaggcag tgcctctctt	600
gggcagtcag atccaccacg tgcttaatat cagggaagaa ggtacttcaa	650
agactctgcc cctgagggtca agagaggatg gggctattca cttttatata	700
tttatataaa attagtagtg agatgtaaaa aaaaaaaaaa aaaa	744

<210> SEQ ID NO 68
 <211> LENGTH: 123
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 68

Met	Ala	Asn	Pro	Gly	Leu	Gly	Leu	Leu	Leu	Ala	Leu	Gly	Leu	Pro
1				5					10					15
Phe	Leu	Leu	Ala	Arg	Trp	Gly	Arg	Ala	Trp	Gly	Gln	Ile	Gln	Thr
				20					25					30
Thr	Ser	Ala	Asn	Glu	Asn	Ser	Thr	Val	Leu	Pro	Ser	Ser	Thr	Ser
				35					40					45
Ser	Ser	Ser	Asp	Gly	Asn	Leu	Arg	Pro	Glu	Ala	Ile	Thr	Ala	Ile
				50					55					60
Ile	Val	Val	Phe	Ser	Leu	Leu	Ala	Ala	Leu	Leu	Leu	Ala	Val	Gly
				65					70					75
Leu	Ala	Leu	Leu	Val	Arg	Lys	Leu	Arg	Glu	Lys	Arg	Gln	Thr	Glu
				80					85					90
Gly	Thr	Tyr	Arg	Pro	Ser	Ser	Glu	Glu	Gln	Phe	Ser	His	Ala	Ala
				95					100					105
Glu	Ala	Arg	Ala	Pro	Gln	Asp	Ser	Lys	Glu	Thr	Val	Gln	Gly	Cys
				110					115					120

Leu Pro Ile

<210> SEQ ID NO 69
 <211> LENGTH: 3265
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 69

gccaggaata actagagagg aacaatgggg ttattcagag gttttgtttt	50
cctcttagtt ctgtgcctgc tgcaccagtc aaatacttcc ttcattaagc	100
tgaataataa tggctttgaa gatattgtca ttgttataga tcctagtgtg	150
ccagaagatg aaaaaataat tgaacaaata gaggatatgg tgactacagc	200
ttctacgtac ctgtttgaag ccacagaaaa aagatttttt ttcaaaaatg	250
tatctatatt aattcctgag aattggaagg aaaatcctca gtacaaaagg	300
cctctacatg aaaaccataa acatgctgat gttatagttg caccacctac	350
actcccaggt agagatgaac catacaccaa gcagttcaca gaatgtggag	400
agaaaggcga atacattcac ttcacccctg accttctact tggaaaaaaa	450
caaaatgaat atggaccacc aggcaaaactg tttgtccatg agtgggctca	500
cctccggtgg ggagtgtttg atgagtacaa tgaagatcag cctttctacc	550
gtgctaagtc aaaaaaaatc gaagcaacaa ggtgttccgc aggtatctct	600
ggtagaataa gagtttataa gtgtcaagga ggcagctgtc ttagtagagc	650

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atgcagaatt gattctacaa caaaactgta tggaaaagat tgtcaattct	700
ttcctgataa agtacaaca gaaaaagcat ccataatgtt tatgcaaagt	750
attgattctg ttgttgaatt ttgtaacgaa aaaaccata atcaagaagc	800
tccaagccta caaaacataa agtgcaatth tagaagtaca tgggaggtga	850
ttagcaattc tgaggatttt aaaaacacca taccatgtgt gacaccacct	900
cctccacctg tcttctcatt gctgaagatc agtcaaagaa ttgtgtgctt	950
agttcttgat aagtctggaa gcatggggg taaggaccgc ctaaatcgaa	1000
tgaatcaagc agcaaaacat ttcctgctgc agactgttga aaatggatcc	1050
tgggtgggga tggttcactt tgatagtact gccactattg taaataagct	1100
aatccaaata aaaagcagtg atgaaagaaa cactctcatg gcaggattac	1150
ctacatatcc tctgggagga acttccatct gctctggaat taaatatgca	1200
tttcaggtga ttggagagct acattcccaa ctcgatggat ccgaagtact	1250
gctgctgact gatggggagg ataacactgc aagttcttgt attgatgaag	1300
tgaacaaga tggggccatt gttcatttta ttgctttggg aagagctgct	1350
gatgaagcag taatagagat gagcaagata acaggaggaa gtcattttta	1400
tgtttcagat gaagctcaga acaatggcct cattgatgct tttggggctc	1450
ttacatcagg aaatactgat ctctcccaga agtcccttca gtcgaaagt	1500
aagggattaa cactgaatag taatgcctgg atgaacgaca ctgtcataat	1550
tgatagtaca gtgggaaagg acacgttctt tctcatcaca tggaaagtc	1600
tgctctccag tatttctctc tgggatccca gtggaacaat aatggaaaat	1650
ttcacagtgg atgcaacttc caaaatggcc tatctcagta ttccaggaa	1700
tgcaaagggt ggcacttggg catacaatct tcaagccaaa gcgaaccag	1750
aaacattaac tattacagta acttctcgag cagcaaattc ttctgtgcct	1800
ccaatcacag tgaatgctaa aatgaataag gacgtaaaca gtttccccag	1850
cccaatgatt gtttacgcag aaattctaca aggatatgta cctgttcttg	1900
gagccaatgt gactgctttc attgaatcac agaattggaca tacagaagtt	1950
ttggaacttt tggataatgg tgcaggcgct gattctttca agaattgatg	2000
agtctactcc aggtatttta cagcatatac agaaaatggc agatatagct	2050
taaaagttcg ggctcatgga ggagcaaaca ctgccaggct aaaattacgg	2100
cctccactga atagagccgc gtacatacca ggctgggtag tgaacgggga	2150
aattgaagca aaccgccaa gacctgaaat tgatgaggat actcagacca	2200
ccttgaggga tttcagccga acagcatccg gaggtgcatt tgtggtatca	2250
caagtcccaa gccttccctt gcctgaccaa taccaccaa gtcaaatcac	2300
agaccttgat gccacagttc atgaggataa gattattctt acatggacag	2350
caccaggaga taattttgat gttggaaaag ttcaacgtta tatcataaga	2400
ataagtgcga gtattcttga tctaagagac agttttgatg atgctcttca	2450
agtaaatact actgatctgt caccaaagga ggccaactcc aaggaaagct	2500
ttgcatttaa accagaaaat atctcagaag aaaatgcaac ccacatattt	2550
attgccatta aaagtataga taaaagcaat ttgacatcaa aagtatccaa	2600

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cattgcacaa gtaactttgt ttatccctca agcaaactct gatgacattg	2650
atcctacacc tactcctact cctactccta ctcttgataa aagtcataat	2700
tctggagtta atattttctac gctgggtattg tctgtgattg ggtctgttgt	2750
aattgttaac tttatttttaa gtaccacccat ttgaacctta acgaagaaaa	2800
aaatcttcaa gtagacctag aagagagttt taaaaaacia aacaatgtaa	2850
gtaaaggata tttctgaatc ttaaaattca tcccatgtgt gatcataaac	2900
tcataaaaaat aattttaaga tgtcggaaaa ggatactttg attaaataaa	2950
aacactcatg gatatgtaaa aactgtcaag attaaaattt aatagtttca	3000
tttatttgtt attttatttg taagaaatag tgatgaacaa agatcctttt	3050
tcatactgat acctggttgt atattatttg atgcaacagt tttctgaaat	3100
gatatttcaa attgcatcaa gaaattaaaa tcacttatct gagtagtcaa	3150
aatacaagta aaggagagca aataaacaac atttggaanaaaaaaaaaa	3200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	3250
aaaaaaaaaa aaaaaa	3265

<210> SEQ ID NO 70

<211> LENGTH: 919

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 70

Met Gly Leu Phe Arg Gly Phe Val Phe Leu Leu Val Leu Cys Leu	1	5	10	15
Leu His Gln Ser Asn Thr Ser Phe Ile Lys Leu Asn Asn Asn Gly	20	25	30	
Phe Glu Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp	35	40	45	
Glu Lys Ile Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser	50	55	60	
Thr Tyr Leu Phe Glu Ala Thr Glu Lys Arg Phe Phe Phe Lys Asn	65	70	75	
Val Ser Ile Leu Ile Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr	80	85	90	
Lys Arg Pro Lys His Glu Asn His Lys His Ala Asp Val Ile Val	95	100	105	
Ala Pro Pro Thr Leu Pro Gly Arg Asp Glu Pro Tyr Thr Lys Gln	110	115	120	
Phe Thr Glu Cys Gly Glu Lys Gly Glu Tyr Ile His Phe Thr Pro	125	130	135	
Asp Leu Leu Leu Gly Lys Lys Gln Asn Glu Tyr Gly Pro Pro Gly	140	145	150	
Lys Leu Phe Val His Glu Trp Ala His Leu Arg Trp Gly Val Phe	155	160	165	
Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg Ala Lys Ser Lys	170	175	180	
Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser Gly Arg Asn	185	190	195	
Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg Ala Cys	200	205	210	
Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln Phe				

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215					220					225				
Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met
				230					235					240
Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His
				245					250					255
Asn	Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg
				260					265					270
Ser	Thr	Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr
				275					280					285
Ile	Pro	Met	Val	Thr	Pro	Pro	Pro	Pro	Pro	Val	Phe	Ser	Leu	Leu
				290					295					300
Lys	Ile	Ser	Gln	Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly
				305					310					315
Ser	Met	Gly	Gly	Lys	Asp	Arg	Leu	Asn	Arg	Met	Asn	Gln	Ala	Ala
				320					325					330
Lys	His	Phe	Leu	Leu	Gln	Thr	Val	Glu	Asn	Gly	Ser	Trp	Val	Gly
				335					340					345
Met	Val	His	Phe	Asp	Ser	Thr	Ala	Thr	Ile	Val	Asn	Lys	Leu	Ile
				350					355					360
Gln	Ile	Lys	Ser	Ser	Asp	Glu	Arg	Asn	Thr	Leu	Met	Ala	Gly	Leu
				365					370					375
Pro	Thr	Tyr	Pro	Leu	Gly	Gly	Thr	Ser	Ile	Cys	Ser	Gly	Ile	Lys
				380					385					390
Tyr	Ala	Phe	Gln	Val	Ile	Gly	Glu	Leu	His	Ser	Gln	Leu	Asp	Gly
				395					400					405
Ser	Glu	Val	Leu	Leu	Leu	Thr	Asp	Gly	Glu	Asp	Asn	Thr	Ala	Ser
				410					415					420
Ser	Cys	Ile	Asp	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile	Val	His	Phe
				425					430					435
Ile	Ala	Leu	Gly	Arg	Ala	Ala	Asp	Glu	Ala	Val	Ile	Glu	Met	Ser
				440					445					450
Lys	Ile	Thr	Gly	Gly	Ser	His	Phe	Tyr	Val	Ser	Asp	Glu	Ala	Gln
				455					460					465
Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Thr	Ser	Gly	Asn
				470					475					480
Thr	Asp	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Leu	Glu	Ser	Lys	Gly	Leu
				485					490					495
Thr	Leu	Asn	Ser	Asn	Ala	Trp	Met	Asn	Asp	Thr	Val	Ile	Ile	Asp
				500					505					510
Ser	Thr	Val	Gly	Lys	Asp	Thr	Phe	Phe	Leu	Ile	Thr	Trp	Asn	Ser
				515					520					525
Leu	Pro	Pro	Ser	Ile	Ser	Leu	Trp	Asp	Pro	Ser	Gly	Thr	Ile	Met
				530					535					540
Glu	Asn	Phe	Thr	Val	Asp	Ala	Thr	Ser	Lys	Met	Ala	Tyr	Leu	Ser
				545					550					555
Ile	Pro	Gly	Thr	Ala	Lys	Val	Gly	Thr	Trp	Ala	Tyr	Asn	Leu	Gln
				560					565					570
Ala	Lys	Ala	Asn	Pro	Glu	Thr	Leu	Thr	Ile	Thr	Val	Thr	Ser	Arg
				575					580					585
Ala	Ala	Asn	Ser	Ser	Val	Pro	Pro	Ile	Thr	Val	Asn	Ala	Lys	Met
				590					595					600
Asn	Lys	Asp	Val	Asn	Ser	Phe	Pro	Ser	Pro	Met	Ile	Val	Tyr	Ala
				605					610					615

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Glu Ile Leu Gln Gly Tyr Val Pro Val	Leu Gly Ala Asn Val Thr
620	625 630
Ala Phe Ile Glu Ser Gln Asn Gly His Thr Glu Val Leu Glu Leu	
635	640 645
Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys Asn Asp Gly Val	
650	655 660
Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly Arg Tyr Ser	
665	670 675
Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg Leu Lys	
680	685 690
Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp Val	
695	700 705
Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp	
710	715 720
Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser	
725	730 735
Gly Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro	
740	745 750
Asp Gln Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val	
755	760 765
His Glu Asp Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn	
770	775 780
Phe Asp Val Gly Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala	
785	790 795
Ser Ile Leu Asp Leu Arg Asp Ser Phe Asp Asp Ala Leu Gln Val	
800	805 810
Asn Thr Thr Asp Leu Ser Pro Lys Glu Ala Asn Ser Lys Glu Ser	
815	820 825
Phe Ala Phe Lys Pro Glu Asn Ile Ser Glu Glu Asn Ala Thr His	
830	835 840
Ile Phe Ile Ala Ile Lys Ser Ile Asp Lys Ser Asn Leu Thr Ser	
845	850 855
Lys Val Ser Asn Ile Ala Gln Val Thr Leu Phe Ile Pro Gln Ala	
860	865 870
Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr Pro Thr Pro Thr Pro	
875	880 885
Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser Thr Leu	
890	895 900
Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile Leu	
905	910 915

Ser Thr Thr Ile

<210> SEQ ID NO 71
 <211> LENGTH: 3877
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien
 <400> SEQUENCE: 71

ctccttaggt ggaaaccctg ggagtagagt actgacagca aagaccggga	50
aagaccatac gtcccgggc aggggtgaca acaggtgtca tctttttgat	100
ctcgtgtgtg gctgccttcc tatttcaagg aaagacgccca aggtaatttt	150
gaccacagag agcaatgatg tagccacctc ctaaccttcc cttcttgaac	200

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ccccagttat gccaggattt actagagagt gtcaactcaa ccagcaagcg	250
gctccttcgg cttacttgt ggttgaggga gagaaccttt gtggggctgc	300
gttctcttag cagtgcctcag aagtgacttg cctgagggtg gaccagaaga	350
aaggaaaggt cccctcttgc tgttggtgc acatcaggaa ggctgtgatg	400
ggaatgaagg tgaacttg gagatttcac ttcagtcatt gcttctgcct	450
gcaagatcat cctttaaaag tagagaagct gctctgtgtg gtggttaact	500
ccaagaggca gaactcgttc tagaaggaaa tggatgcaag cagctccggg	550
ggcccaaac gcatgcttcc tgtggtctag cccagggaag cccttccgtg	600
ggggcccg ctttgaggga tggccacggg tctggacgca tggctgattc	650
ctgaatgatg atggttcgcc gggggctgct tgcgtggatt tcccggttg	700
tggttttgct ggtgctcctc tgctgtgcta tctctgtcct gtacatgttg	750
gcctgcaccc caaaagggtga cgaggagcag ctggcactgc ccagggccaa	800
cagccccacg gggaaggagg ggtaccaggc cgtccttcag gaggggagg	850
agcagcaccg caactacgtg agcagcctga agcggcagat cgcacagctc	900
aaggaggagc tgcaggagag gagtgcagcag ctgaggaatg ggcagtacca	950
agccagcgat gctgctggcc tgggtctgga caggagcccc ccagagaaaa	1000
cccaggccga cctcctggcc ttcctgcact cgcagggtgga caaggcagag	1050
gtgaatgctg gcgtcaagct ggccacagag tatgcagcag tgcctttcga	1100
tagctttact ctacagaagg tgtaccagct ggagactggc cttaccggcc	1150
accccgagga gaagcctgtg aggaaggaca agcgggatga gttggtggaa	1200
gccattgaat cagccttgga gaccctgaac aatcctgcag agaacagccc	1250
caatcaccgt ccttacacgg cctctgattt catagaaggg atctaccgaa	1300
cagaaaggga caaagggaca ttgtatgagc tcaccttcaa aggggaccac	1350
aaacacgaat tcaaacggct catcttattt cgaccattca gccccatcat	1400
gaaagtgaat aatgaaaagc tcaacatggc caacacgctt atcaatgtta	1450
tcgtgcctct agcaaaaagg gtggacaagt tccggcagtt catgcagaat	1500
ttcagggaga tgtgcattga gcaggatggg agagtccatc tactgttgt	1550
ttactttggg aaagaagaaa taaatgaagt caaaggaata cttgaaaaa	1600
cttccaaagc tgccaacttc aggaacttta ccttcattca gctgaatgga	1650
gaattttctc ggggaaaggg acttgatgtt ggagcccgtc tctggaaggg	1700
aagcaacgtc cttctctttt tctgtgatgt ggacatctac ttcacatctg	1750
aattcctcaa tacgtgtagg ctgaatacac agccagggaa gaaggatatt	1800
tatccagtgc ttttcagtca gtacaatcct ggcataatat acggccacca	1850
tgatgcagtc cctcccttgg aacagcagct ggtcataaag aaggaaactg	1900
gattttggag agactttgga tttgggatga cgtgtcagta tcggtcagac	1950
ttcatcaata taggtgggtt tgatctggac atcaaaggct ggggaggaga	2000
ggatgtgcac ctttatcgca agtatctcca cagcaacctc atagtgttac	2050
ggacgcctgt gcgaggactc tccacctct ggcatgagaa gcgctgcatg	2100
gacgagctga ccccgagca gtacaagatg tgcattgcagt ccaaggccat	2150
gaacgaggca tcccacggcc agctgggcat gctggtgttc aggcacgaga	2200

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tagaggctca ccttcgcaaa cagaaacaga agacaagtag caaaaaaaca	2250
tgaactccca gagaaggatt gtgggagaca ctttttcttt ctttttgcaa	2300
ttactgaaag tggctgcaac agagaaaaga cttccataaa ggacgacaaa	2350
agaattggac tgatgggtca gagatgagaa agcctccgat ttctctctgt	2400
tgggcttttt acaacagaaa tcaaaatctc cgctttgcct gcaaaagtaa	2450
cccagttgca ccctgtgaag tgtctgacaa aggcagaatg cttgtgagat	2500
tataagccta atgggtgtga ggttttgatg gtgtttacaa tacactgaga	2550
cctgttgttt tgtgtgctca ttgaaatatt catgatttaa gagcagtttt	2600
gtaaaaaatt cattagcatg aaaggcaagc atatttctcc tcatatgaat	2650
gagcctatca gcagggtctt agtttctagg aatgctaaaa tatcagaagg	2700
caggagagga gataggctta ttatgatact agtgagtaca ttaagtaaaa	2750
taaaatggac cagaaaagaa aagaaccat aaatatcgtg tcatattttc	2800
cccaagatta accaaaaata atctgcttat ctttttggtt gtccttttaa	2850
ctgtctccgt ttttttcttt tatttaaaaa tgcacttttt ttcccttggtg	2900
agttatagtc tgcttattta attaccactt tgcaagcctt acaagagagc	2950
acaagttggc ctacattttt atatttttta agaagatact ttgagatgca	3000
ttatgagaac tttcagttca aagcatcaaa ttgatgccat atccaaggac	3050
atgccaatg ctgattctgt caggcactga atgtcaggca ttgagacata	3100
gggaaggaat ggtttgact aatacagacg tacagatact ttctctgaag	3150
agtattttcg aagaggagca actgaacact ggaggaaaag aaaatgacac	3200
tttctgcttt acagaaaagg aaactcattc agactggtga tatcgtgatg	3250
tacctaaaag tcagaaacca cattttctcc tcagaagtag ggaccgcttt	3300
cttacctgtt taaataaacc aaagtatacc gtgtgaacca aacaatctct	3350
tttcaaaaca gggtgctcct cctggcttct ggcttcata agaagaaatg	3400
gagaaaaata tatatatata tatatatatt gtgaaagatc aatccatctg	3450
ccagaatcta gtgggatgga agtttttgct acatgttatc caccacaggc	3500
caggtggaag taactgaatt attttttaaa ttaagcagtt ctactcaatc	3550
accaagatgc ttctgaaaat tgcattttat taccatttca aactattttt	3600
taaaaataaa tacagttaac atagagtggg ttcttcattc atgtgaaaat	3650
tattagccag caccagatgc atgagctaata tatctctttg agtccttgct	3700
tctgtttgct cacagtaaac tcattgttta aaagcttcaa gaacattcaa	3750
gctgttggtg tgtaaaaaa tgcattgtat tgatttgtac tggtagttta	3800
tgaaatttaa ttaaaacaca ggccatgaat ggaagggtgg attgcacagc	3850
taataaaata tgatttgggt atatgaa	3877

<210> SEQ ID NO 72

<211> LENGTH: 532

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 72

Met	Met	Met	Val	Arg	Arg	Gly	Leu	Leu	Ala	Trp	Ile	Ser	Arg	Val
1					5				10					15

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Val Val Leu Leu Val Leu Leu Cys Cys Ala Ile Ser Val Leu Tyr	20	25	30
Met Leu Ala Cys Thr Pro Lys Gly Asp Glu Glu Gln Leu Ala Leu	35	40	45
Pro Arg Ala Asn Ser Pro Thr Gly Lys Glu Gly Tyr Gln Ala Val	50	55	60
Leu Gln Glu Trp Glu Glu Gln His Arg Asn Tyr Val Ser Ser Leu	65	70	75
Lys Arg Gln Ile Ala Gln Leu Lys Glu Glu Leu Gln Glu Arg Ser	80	85	90
Glu Gln Leu Arg Asn Gly Gln Tyr Gln Ala Ser Asp Ala Ala Gly	95	100	105
Leu Gly Leu Asp Arg Ser Pro Pro Glu Lys Thr Gln Ala Asp Leu	110	115	120
Leu Ala Phe Leu His Ser Gln Val Asp Lys Ala Glu Val Asn Ala	125	130	135
Gly Val Lys Leu Ala Thr Glu Tyr Ala Ala Val Pro Phe Asp Ser	140	145	150
Phe Thr Leu Gln Lys Val Tyr Gln Leu Glu Thr Gly Leu Thr Arg	155	160	165
His Pro Glu Glu Lys Pro Val Arg Lys Asp Lys Arg Asp Glu Leu	170	175	180
Val Glu Ala Ile Glu Ser Ala Leu Glu Thr Leu Asn Asn Pro Ala	185	190	195
Glu Asn Ser Pro Asn His Arg Pro Tyr Thr Ala Ser Asp Phe Ile	200	205	210
Glu Gly Ile Tyr Arg Thr Glu Arg Asp Lys Gly Thr Leu Tyr Glu	215	220	225
Leu Thr Phe Lys Gly Asp His Lys His Glu Phe Lys Arg Leu Ile	230	235	240
Leu Phe Arg Pro Phe Ser Pro Ile Met Lys Val Lys Asn Glu Lys	245	250	255
Leu Asn Met Ala Asn Thr Leu Ile Asn Val Ile Val Pro Leu Ala	260	265	270
Lys Arg Val Asp Lys Phe Arg Gln Phe Met Gln Asn Phe Arg Glu	275	280	285
Met Cys Ile Glu Gln Asp Gly Arg Val His Leu Thr Val Val Tyr	290	295	300
Phe Gly Lys Glu Glu Ile Asn Glu Val Lys Gly Ile Leu Glu Asn	305	310	315
Thr Ser Lys Ala Ala Asn Phe Arg Asn Phe Thr Phe Ile Gln Leu	320	325	330
Asn Gly Glu Phe Ser Arg Gly Lys Gly Leu Asp Val Gly Ala Arg	335	340	345
Phe Trp Lys Gly Ser Asn Val Leu Leu Phe Phe Cys Asp Val Asp	350	355	360
Ile Tyr Phe Thr Ser Glu Phe Leu Asn Thr Cys Arg Leu Asn Thr	365	370	375
Gln Pro Gly Lys Lys Val Phe Tyr Pro Val Leu Phe Ser Gln Tyr	380	385	390
Asn Pro Gly Ile Ile Tyr Gly His His Asp Ala Val Pro Pro Leu	395	400	405

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Glu	Gln	Gln	Leu	Val	Ile	Lys	Lys	Glu	Thr	Gly	Phe	Trp	Arg	Asp
			410						415					420
Phe	Gly	Phe	Gly	Met	Thr	Cys	Gln	Tyr	Arg	Ser	Asp	Phe	Ile	Asn
			425						430					435
Ile	Gly	Gly	Phe	Asp	Leu	Asp	Ile	Lys	Gly	Trp	Gly	Gly	Glu	Asp
			440						445					450
Val	His	Leu	Tyr	Arg	Lys	Tyr	Leu	His	Ser	Asn	Leu	Ile	Val	Val
			455						460					465
Arg	Thr	Pro	Val	Arg	Gly	Leu	Phe	His	Leu	Trp	His	Glu	Lys	Arg
			470						475					480
Cys	Met	Asp	Glu	Leu	Thr	Pro	Glu	Gln	Tyr	Lys	Met	Cys	Met	Gln
			485						490					495
Ser	Lys	Ala	Met	Asn	Glu	Ala	Ser	His	Gly	Gln	Leu	Gly	Met	Leu
			500						505					510
Val	Phe	Arg	His	Glu	Ile	Glu	Ala	His	Leu	Arg	Lys	Gln	Lys	Gln
			515						520					525
Lys	Thr	Ser	Ser	Lys	Lys	Thr								
			530											

<210> SEQ ID NO 73
 <211> LENGTH: 1701
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien
 <220> FEATURE:
 <221> NAME/KEY: unsure
 <222> LOCATION: 1528
 <223> OTHER INFORMATION: unknown base

<400> SEQUENCE: 73

gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt	50
tgctcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc	100
tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacact	150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc	200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtccect	250
gcaccccttc ctgggacact atgttggtct ccgccctcct gctggagggtg	300
atttgatcc tgggtgcaga tgggggtcaa cactggacgt atgagggccc	350
acatggtcag gaccattggc cagcctctta cctgagtggt ggaacaatg	400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat	450
ttgctgctc tgcagcccca cgcatatgac cagcctggca ccgagccttt	500
ggacctgcac aacaatggcc acacagtgc actctctctg ccctctaccc	550
tgtatctggg tggacttccc cgaaaatatg tagctgccca gctccacctg	600
cactggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag	650
tgaagccaca ttgcagagc tccacattgt acattatgac tctgattcct	700
atgacagctt gactgaggct gctgagaggc ctcagggcct ggctgtcctg	750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat	800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc	850
ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc	900
cgctacaatg gctcgctcac aactcccct tgctaccaga gtgtgctctg	950
gacagttttt tatagaaggt ccagatttc aatggaacag ctggaaaagc	1000

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ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta	1050
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc	1100
tttcaccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag	1150
gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatttc	1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt	1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac	1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg	1350
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct	1400
ccttcccctg gacatctctt agagaggaat ggaccacaggc tgtcattcca	1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag	1500
gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg	1550
gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc	1600
tttccctaga tatactgcgg gatctctcct taggataaag agttgctgtt	1650
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt	1700
t	1701

<210> SEQ ID NO 74

<211> LENGTH: 337

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 74

Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala	1	5	10	15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln	20	25	30	
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln	35	40	45	
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp	50	55	60	
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu	65	70	75	
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu	80	85	90	
Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala	95	100	105	
Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly	110	115	120	
Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His	125	130	135	
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala	140	145	150	
Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu	155	160	165	
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His	170	175	180	
Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro	185	190	195	
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe	200	205	210	

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Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val
 215 220 225

Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
 230 235 240

Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro
 245 250 255

Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn
 260 265 270

Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr
 275 280 285

Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly
 290 295 300

Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile
 305 310 315

Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser
 320 325 330

Ala Gln Ala Thr Thr Glu Ala
 335

<210> SEQ ID NO 75

<211> LENGTH: 1743

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 75

tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg	50
gcagttccct gtgtctctgg tggttgcct aaacctgcaa acatcacctt	100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc	150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg	200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgctc	250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc	300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac	350
taaatcaaac agaactgtgt cccagtgtgt gaccaaccac acgctgggtc	400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc	450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag	500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggg	550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat	600
tccactacc gatatatcca cgttggcaaa gagaacacc cagcaaattt	650
gattttgatt tatgaaatg aatttgacaa aagattcttt gtgcctgctg	700
aaaaaatcgt gattaacttt atcaccccca atatctcgga tgattctaaa	750
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag	800
ccttaatgat cctcagccca gcgggaacct gagggccct caggaggaag	850
aggagtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt	900
gactctgaag aaaacacgga aggtacttct ctcaccacgc aagagtcctt	950
cagcagaaca atacccccg ataaaacagt cattgaatat gaatatgatg	1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg	1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcgtt	1100

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ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc      1150
aagacttaga ccccctggcg caggagcaca cagactcgga ggagggggccg      1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag      1250
gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg      1300
agccttctga gggggatggg ctcgagagag agggctcttct atctagactc      1350
tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct      1400
catgcaattc atggaggaat gggggttata tgtgcagatg gaaaactgat      1450
gccaacactt ccttttgctt ttgttttcct gtgcaacaaa gtgagtcacc      1500
cctttgatcc cagccataaa gtacctggga tgaagaagt tttttccagt      1550
ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca      1600
cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atgggtgggc      1650
tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat      1700
aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt      1743

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<210> SEQ ID NO 76

<211> LENGTH: 442

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 76

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Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys
  1             5             10             15
Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
             20             25             30
Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
             35             40             45
Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
             50             55             60
Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
             65             70             75
Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
             80             85             90
Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
             95             100            105
His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
             110            115            120
Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
             125            130            135
Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
             140            145            150
Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
             155            160            165
Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
             170            175            180
Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
             185            190            195
Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
             200            205            210
Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
             215            220            225

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Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
 230 235 240
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
 245 250 255
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
 260 265 270
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
 275 280 285
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
 290 295 300
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
 305 310 315
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
 320 325 330
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
 335 340 345
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
 350 355 360
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
 365 370 375
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
 380 385 390
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
 395 400 405
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
 410 415 420
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
 425 430 435
 Leu Tyr Val Gln Met Glu Asn
 440

<210> SEQ ID NO 77

<211> LENGTH: 1636

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 77

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt	50
gctgccctct gacacctggg aagatggccg gcccgtagac cttaccctt	100
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtccac	150
tgcatgtctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg	200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc	250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct	300
ggtgaacacc gtctgaagc acatcatctg gctgaagtc atcacagcta	350
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta	400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaaa	450
gaccatcgtg gaggttccaca tgacgactga ggcccaagcc accatccgca	500
tggaacaccag tgcaagtggc cccacccgcc tggtcctcag tgactgtgcc	550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttct	600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc	650

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ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat	700
ggcatgtatg cagacctcct gcagctgggt aaggtgcccc tttccctcag	750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca	800
ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaagggtg	850
accaagtggt tcaataactc tgcagcttcc ctgacaatgc ccaccctgga	900
caacatcccg ttcagcctca tcgtgagtca ggacgtgggt aaagctgcag	950
tgggtgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg	1000
cttctcgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga	1050
aaaggctgca gataagctgg gatctacca gatcgtgaag atcctaactc	1100
aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa	1150
ctgatcgtgc tggaaagtgt tccctccagt gaagccctcc gccctttgtt	1200
caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg	1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg	1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat	1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa	1400
gatctgggggt cccagtgtca ttggtgaagg ccttgggatt cgaggcagct	1450
gagtcctcac tgaccaagga tgccttgtg cttactccag cctccttggtg	1500
gaaaccagc tctcctgtct cccagtgaag acttggatgg cagccatcag	1550
ggaaggctgg gtcccagctg ggagtatgg tgtgagctct atagaccatc	1600
cctctctgca atcaataaac acttgctgtg gaaaaa	1636

<210> SEQ ID NO 78

<211> LENGTH: 484

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 78

Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala	
1 5 10 15	
Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile	
20 25 30	
Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys	
35 40 45	
Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser	
50 55 60	
Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser	
65 70 75	
Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile	
80 85 90	
Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp	
95 100 105	
Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe	
110 115 120	
Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr	
125 130 135	
Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro	
140 145 150	

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Thr Arg Leu Val	Leu Ser Asp Cys Ala	Thr Ser His Gly Ser Leu
	155	160 165
Arg Ile Gln Leu	Leu Tyr Lys Leu Ser	Phe Leu Val Asn Ala Leu
	170	175 180
Ala Lys Gln Val	Met Asn Leu Leu Val	Pro Ser Leu Pro Asn Leu
	185	190 195
Val Lys Asn Gln	Leu Cys Pro Val Ile	Glu Ala Ser Phe Asn Gly
	200	205 210
Met Tyr Ala Asp	Leu Leu Gln Leu Val	Lys Val Pro Ile Ser Leu
	215	220 225
Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile Lys
	230	235 240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp Ser
	245	250 255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser Leu
	260	265 270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val Ser
	275	280 285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro Glu
	290	295 300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala His
	305	310 315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala Asp
	320	325 330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp Thr
	335	340 345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln Leu
	350	355 360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro Leu
	365	370 375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr Thr
	380	385 390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser Asp
	395	400 405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro Asp
	410	415 420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu Leu
	425	430 435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser Leu
	440	445 450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr Lys
	455	460 465
Asp Ala Leu Val	Leu Thr Pro Ala Ser	Leu Trp Lys Pro Ser Ser
	470	475 480
Pro Val Ser Gln		

<210> SEQ ID NO 79

<211> LENGTH: 1475

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 79

gagagaagtc agcctggcag agagactctg aaatgagggg ttagaggtgt

50

tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac

100

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gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtagg      150
ctacatccta ggcccttctgg ggcttttggg cacactgggt gccatgctgc      200
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca      250
gttggtctct ccaagggcct ctggatggaa tgtgccacac acagcacagg      300
catcaccacg tgtgacatct atagcaccct tctgggcctg cccgctgaca      350
tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctccctccctg      400
gcctgcatta tctctgtggt ggcatgaga tgcacagtct tctgccagga      450
atcccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc      500
ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc      550
ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat      600
tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag      650
ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac      700
tactacgatg cctaccaagc ccaacctctt gccacaagga gctctccaag      750
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga      800
cagggtatgt gtgaagaacc aggggccaga gctggggggg ggctgggtct      850
gtgaaaaaca gtggacagca ccccaggggc cacagggtgag ggacactacc      900
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt      950
ggattgagca aaggcagaaa tgggggctag tgtaacagca tgcagggtga     1000
attgccaaag atgctcgcca tgccagcctt tctgttttcc tcaccttgct     1050
gtcccccctgc cctaagtccc caaccctcaa cttgaaaccc cattccctta     1100
agccaggact cagaggatcc ctttgccttc tggtttacct gggactccat     1150
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga     1200
ccctctctct ggctgaggtt ggctcttagc tcattgctgg ggatgggaag     1250
gagaagcagt ggcttttgtg ggcattgctc taacctactt ctcaagcttc     1300
cctccaaaga aactgattgg ccctggaacc tccatcccac tcttgttatg     1350
actccacagt gtccagacta atttgtgcat gaactgaaat aaaaccatcc     1400
tacggtatcc agggaacaga aagcaggatg caggatggga ggacaggaag     1450
gcagcctggg acatttaaaa aaata                                     1475

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<210> SEQ ID NO 80

<211> LENGTH: 230

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 80

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Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
  1             5             10            15
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
             20             25            30
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
             35             40            45
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly
             50             55            60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
             65             70            75

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Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
 80 85 90
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
 95 100 105
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala
 110 115 120
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
 125 130 135
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
 140 145 150
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
 155 160 165
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
 170 175 180
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
 185 190 195
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
 200 205 210
 Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
 215 220 225
 Leu Thr Gly Tyr Val
 230

<210> SEQ ID NO 81

<211> LENGTH: 1732

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 81

cccacgcgtc cgcgcctctc ccttctgctg gaccttcctt cgtctctcca	50
ttctctccctc ctttccccgc gttctctttc cacctttctc ttcttcccac	100
cttagacctc ccttctgccc ctcttttctt gcccacgct gcttctgggc	150
ccttctccga ccccgcctcta gcagcagacc tctgggggtc tgtgggttga	200
tctgtggccc ctgtgectcc gtgtcctttt cgtctccctt cctcccgact	250
ccgctcccg accagcgggc tgacctggg gaaaggatgg ttcccagggt	300
gagggtcctc tcctccttgc tgggactcgc gctgctctgg tccccctgg	350
actcccacgc tcgagcccgc ccagacatgt tctgcctttt ccatgggaag	400
agatactccc ccggcgagag ctggcacccc tacttgagac cacaaggcct	450
gatgtactgc ctgcgtgta cctgctcaga gggcgcccat gtgagttgtt	500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca	550
cagcaatgct gtcccagtg tgtggaacct cacttcct ctggactccg	600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag	650
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt	700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg	750
ccccgaacca ggctgcccag caccctctcc actgccagac tcctgctgcc	800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg	850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc	900
tgggagaaaag agaggcccgg gcacccacgc cccactggc ctcagcgccc	950

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ctctgagcctt catccctcgc cacttcagac ccaagggagc aggcagcaca	1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg	1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct	1100
tcggccccctt gccctgcac cctatgcacct gtgaggatgg ccgccaggac	1150
tgccagcgtg tgacctgtcc caccgagtac cctgcccgtc accccgagaa	1200
agtggctggg aagtgcctgca agatttggcc agaggacaaa gcagaccctg	1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc	1300
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc	1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg	1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggccaagg	1450
ccacacagcc agaattcttc acttgactca gatcaagaaa gtcaggaagc	1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac	1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac	1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca	1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg	1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa	1732

<210> SEQ ID NO 82

<211> LENGTH: 451

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 82

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala	1	5	10	15
Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp	20	25	30	
Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser	35	40	45	
Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg	50	55	60	
Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His	65	70	75	
Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln	80	85	90	
Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg	95	100	105	
Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His	110	115	120	
Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro	125	130	135	
Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys	140	145	150	
Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro	155	160	165	
Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu	170	175	180	
Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg	185	190	195	

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His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
 200 205 210
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
 215 220 225
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
 230 235 240
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
 245 250 255
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
 260 265 270
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
 275 280 285
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys
 290 295 300
 Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro
 305 310 315
 Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg
 320 325 330
 Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser
 335 340 345
 Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala
 350 355 360
 Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu
 365 370 375
 Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His
 380 385 390
 Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala
 395 400 405
 Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
 410 415 420
 Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
 425 430 435
 Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
 440 445 450

Thr

<210> SEQ ID NO 83

<211> LENGTH: 2052

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 83

gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgccct 50
 ccgctcacgc agagcctctc cgtggcttcc gcacottgag cattagacca 100
 gttctcctct tctctctaata ccatcogtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacaggagcg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450

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attctattgc ggaggggcgc atctctctga ggctggaaaa cattactgtg	500
ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca	550
gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca	600
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc	650
tcgggctggt tcccccgccc cacagcgaag tggaaagtc cacaaggaca	700
ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgtttg	750
atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt	800
tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat	850
aggagatacc tttttcgagc ctatatctgt gcacctggct accaaagtac	900
tgggaatact ctgctgtggc ctattttttg gcattgttgg actgaagatt	950
ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag	1000
aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg	1050
tgactctgga tccagagacg gctcaccga agctctgcgt ttctgatctg	1100
aaaactgtaa cccatagaaa agctccccag gagtgccctc actctgagaa	1150
gagatttaca aggaagagtg tggtgccctc tcagagtttc caagcaggga	1200
aacattactg ggaggtggac ggaggacaca ataaaaggtg gcgcgtggga	1250
gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc	1300
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca	1350
cattaaatcc ccgttttacc agcgtcttcc ccaggacccc acctacaaaa	1400
ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat	1450
aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat	1500
tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc	1550
atagtcatct gcccagtcac ccaggaatca gagaaaggag cctcttgcca	1600
aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg	1650
caaccacgcc cttcctcccc aggggtgaaa tgtaggatga atcacatccc	1700
acattcttct ttagggatat taaggtctct ctcccagatc caaagtcccg	1750
cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac	1800
atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga	1850
cattacattt agtttgcctc cactccatct ggctaagtga tcttgaaata	1900
ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg	1950
tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg	2000
acagagtgta tcctaattgtt ttgttcatta tattacactt tcagtaaaaa	2050
aa	2052

<210> SEQ ID NO 84

<211> LENGTH: 500

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 84

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly
1				5					10					15

Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala

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20					25					30				
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
				35					40					45
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
				50					55					60
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
				65					70					75
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
				95					100					105
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
				110					115					120
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
				125					130					135
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
				140					145					150
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
				170					175					180
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
				185					190					195
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
				200					205					210
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
				215					220					225
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu
				230					235					240
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys
				245					250					255
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
				320					325					330
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val
				335					340					345
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg	Val	Gly	Val	Cys	Arg	Asp
				350					355					360
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val	Thr	Leu	Ser	Pro	Asp	His
				365					370					375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	Glu	His	Leu	Tyr	Phe	Thr
				380					385					390
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	Arg	Thr	Pro	Pro	Thr
				395					400					405
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	Thr	Ile	Ser	Phe
				410					415					420

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Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg
 425 430 435
 Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn
 440 445 450
 Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu
 455 460 465
 Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu
 470 475 480
 Thr Ser Asn Ser Glu Ser Ser Ser Gln Ala Thr Thr Pro Phe Leu
 485 490 495
 Pro Arg Gly Glu Met
 500

<210> SEQ ID NO 85

<211> LENGTH: 1665

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 85

aacagacggt ccctcgcggc cctggcacct ctaaccccag acatgctgct	50
gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa	100
gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt	150
gtccatgtgc cctgctcctt ctcctacccc tcgcatggct ggatttacct	200
tggcccagta gttcatggct actgggtccg ggaaggggcc aatacagacc	250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag	300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac	350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc	400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct	450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac	500
cctggagtcc ggctgcccc agaattctgac ctgctctgtg ccttgggcct	550
gtgagcaggg gacacccct atgatctcct ggataggac ctccgtgtcc	600
ccccggacc cctccaccac ccgctcctcg gtgctcacc tcattccaca	650
gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctggg	700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct	750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt	800
cctgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgc	850
tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc	900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg	950
ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct	1000
gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc	1050
ctgcagagca aagccacatc aggagtgact cagggggtgg tcgggggagc	1100
tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag	1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat	1200
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc	1250
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag	1300

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cttctgcccc ctcctcagtg ggggaaggag agctccagta tgcacccctc	1350
agcttcacaga tgggtgaagcc ttgggactcg cggggacagg aggccactga	1400
caccgagtagc tcggagatca agatccacag atgagaaaact gcagagactc	1450
accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc	1500
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact	1550
atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc	1600
tcaaacctga atccacactg tgcctccctt tttatTTTTT taactaaaag	1650
acagacaaat tccta	1665

<210> SEQ ID NO 86

<211> LENGTH: 463

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 86

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala	1	5	10	15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr	20	25	30	
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr	50	55	60	
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala	65	70	75	
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg	80	85	90	
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser	95	100	105	
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg	110	115	120	
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu	125	130	135	
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile	140	145	150	
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser	155	160	165	
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp	170	175	180	
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser	185	190	195	
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser	200	205	210	
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn	215	220	225	
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr	230	235	240	
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly	245	250	255	
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu	260	265	270	
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu				

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275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala		
410	415	420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser		
425	430	435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu		
440	445	450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg		
455	460	

<210> SEQ ID NO 87

<211> LENGTH: 1176

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 87

```

agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga      50
aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta      100
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga      150
tggtagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc      200
gtctccatct ctgccagaa gctgcaagga aatcaaagac gaatgtccta      250
gtgcatttga tggcctgtat tttctccgca ctgagaatgg tgttatctac      300
cagaccttct gtgacatgac ctctgggggt ggcggctgga ccctgggtggc      350
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcgatcgct      400
ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac      450
tgggccaaact acaacacctt tggatctgca gaggcggcca cgagcgatga      500
ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct      550
ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg      600
ctgaggtacc gcacggacac tggcttctc cagacactgg gacataatct      650
gtttggcatc taccagaaat atccagttaa atatggagaa ggaagtgtt      700
ggactgacaa cggcccgggtg atccctgtgg tctatgattt tggcgacgcc      750
cagaaaaacag catcttatta ctcaccctat ggccagcggg aattcactgc      800
gggatttgtt cagttcaggg tatttaataa cgagagagca gccaacgcct      850

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tgtgtgctgg aatgaggggc accggatgta acactgagca tcaactgcatt	900
ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt	950
ttctggtttt gattggagtg gatatggaac tcatgttggt tacagcagca	1000
gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt	1050
tgtgggaggg aacccagacc tctcctccca accatgagat cccaaggatg	1100
gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa	1150
taaatcatat tgactcaaga aaaaaa	1176

<210> SEQ ID NO 88

<211> LENGTH: 313

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 88

Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg		
1 5 10 15		
Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr		
20 25 30		
Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys		
35 40 45		
Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr		
50 55 60		
Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly		
65 70 75		
Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met		
80 85 90		
Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly		
95 100 105		
Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr		
110 115 120		
Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys		
125 130 135		
Asn Pro Gly Tyr Tyr Asp Ile Gln Ala Lys Asp Leu Gly Ile Trp		
140 145 150		
His Val Pro Asn Lys Ser Pro Met Gln His Trp Arg Asn Ser Ser		
155 160 165		
Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu Gln Thr Leu Gly		
170 175 180		
His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val Lys Tyr Gly		
185 190 195		
Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro Val Val		
200 205 210		
Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser Pro		
215 220 225		
Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val		
230 235 240		
Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg		
245 250 255		
Val Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Gly		
260 265 270		
Tyr Phe Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly		
275 280 285		

-continued

Phe Asp Trp Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser
290 295 300

Arg Glu Ile Thr Glu Ala Ala Val Leu Leu Phe Tyr Arg
305 310

<210> SEQ ID NO 89

<211> LENGTH: 759

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 89

```
ctagatttgt cggcttgagg ggagacttca ggagtcgctg tctctgaact      50
tccagcctca gagaccgccc cccttgctcc cgagggccat gggccgggtc      100
tcagggtctg tgccctctcg cttcctgacg ctctggcgcg atctgggtgt      150
cgctcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc      200
ctctcacggt cacccccag gagtatgaca agcaggacat tcagctggtg      250
gccgcgtct ctgtcaccct gggcctcttt gcagtggagc tggccggttt      300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg      350
gggtcactg tagtgcatcc gtggccctgt ccttcttcat attcgagcgt      400
tgaggagtga ctacgtattg gtacattttt gtcttctgca gtgcccttcc      450
agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga      500
aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg      550
ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt      600
ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg      650
tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata      700
tgttttgtag taacattaag acttatatac agttttaggg gacaattaa      750
aaaaaaaaa                                         759
```

<210> SEQ ID NO 90

<211> LENGTH: 140

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 90

```
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1          5          10          15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20          25          30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35          40          45
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50          55          60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65          70          75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80          85          90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95          100         105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110         115         120
```


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Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135

Lys Lys Lys Pro Phe
140

<210> SEQ ID NO 91

<211> LENGTH: 1871

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 91

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag	50
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc	100
tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac	150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcggaa	200
gcggggccac atctcaccta agtcccggcc catggccaat tccactctcc	250
tagggctgct ggcgccgctt ggggaggctt ggggcattct tgggcagccc	300
cccaaccgcc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat	350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc	400
tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc	450
cacttccaac acaatgccac agggcaggga aacatctcca tcagcctcgt	500
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcacgt	550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta	600
gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg	650
ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct	700
tcaaagtcgt ctgtgtctac atgcgcttct acagcacgga ctatcggtg	750
gtccagaagg tgtgccaga ttacaactac catagtgata cccctacta	800
cccatctggg tgaccgggg caggccacag agggcaggcc agggctggaa	850
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaagg	900
gttgggcctc aggcaggag gggggtggag acgaggagat gccagtg	950
gccagggcc agtctcaagt gccagagaaa ggggcccaag tgctggctcc	1000
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagt	1050
ggctctctgt gcagcctcac agggccttgc cacggagcca cagagagat	1100
ctgggtcccc gaggcctgtg gccaggccga tcagtgtggc ccagatcaa	1150
gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata	1200
gcaacaggga gggggagatt tcatacgtgt ggacagcctg tcaacttag	1250
atggatggct gagagggctt cctaggagcc agtcagcagg gtgggggtg	1300
gccagaggag ctctccagcc ctgcctagt ggcgccctga gcccttgtc	1350
gtgtgctgag catggcatga ggctgaagt gcaaccctgg ggtctttgat	1400
gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaa	1450
ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca	1500
cccatccta agctaagaca ggacgattgt ggtcctccca cactaaggcc	1550
acagcccac cgcgtgctgt gtgtccctct tccaccccaa cccctgctg	1600
ctcctctggg agcatccatg tcccggagag gggccctca acagtcagcc	1650

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```

tcacctgtca gaccgggggt ctcccggatc tggatggcgc cgcctctca      1700
gcagcgggca cgggtggggc ggggcccggc cgcagagcat gtgctggatc      1750
tggtctgtgt gtctgtctgt ggggtggggg aggggagggg agtcttgtga      1800
aaccgtgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga      1850
aataaagctt gccccggggc a                                     1871

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<210> SEQ ID NO 92
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 92

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```

Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser
 1              5              10              15
Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser
 20             25             30
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35             40             45
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
 50             55             60
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65             70             75
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
 80             85             90
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95            100            105
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
110            115            120
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
125            130            135
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
140            145            150
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
155            160            165
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
170            175            180
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
185            190            195
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
200            205            210
Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215            220            225
Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230            235            240
Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245            250

```

```

<210> SEQ ID NO 93
<211> LENGTH: 902
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

```

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<400> SEQUENCE: 93

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```

cgggtggccat gactgcggcc gtgtttcttc gctgcgcctt cattgccttc      50

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```

gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg      100
tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga      150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat      200
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta      250
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca      300
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga      350
ctgctggcct atgtttcttg ctggggcttt ggaatcatga gtggagtatt      400
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca      450
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg      500
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg      550
tgagaagaaa aagtggggca tcctccttat cgttctctcg acccacctgc      600
tggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg      650
tcagcattta taatcctggt gctcatgggc acctgggcat tcttagctgc      700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga      750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact      800
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc      850
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga      900
ta                                                                902

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<210> SEQ ID NO 94
<211> LENGTH: 257
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 94

```

```

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
  1             5             10            15
Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
 20             25            30
Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
 35             40            45
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
 50             55            60
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
 65             70            75
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
 80             85            90
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
 95            100           105
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110           115           120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125           130           135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140           145           150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155           160           165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly

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170					175					180				
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
				185					190					195
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
				200					205					210
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr
				215					220					225
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
				230					235					240
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg
				245					250					255

Ser Arg

<210> SEQ ID NO 95

<211> LENGTH: 1073

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 95

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aatttttcac cagagtaaacc ttgagaaacc aactggacct tgagtattgt      50
acattttgccc tcgtggacccc aaaggtagca atctgaaaca tgaggagtag      100
gatttctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca      150
aacctgctttt gggactccct cccacaaaac tggctccgga tcaggaaca      200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat      250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaatc      300
ctgctgcagg aatgacacct ggtaccaga cccaccatt gacctggga      350
gggttgaatg tacaacagca actgcaccca catgtgttac caatttttgt      400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac      450
aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatcctg      500
cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc      550
agcaggagga gcaggtgtaa atcctgccac ccagggaacc ccagcaggcc      600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct      650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc      700
agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct      750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata      800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct      850
gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa      900
cttttaaaaa caataattca atggataaat ctgtctttga aatataacat      950
tatgtgcctt ggatgatatg catattaaaa catatttgga aaactggaaa     1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     1050
aaaaaaaaaa aaaaaaaaaa aaa                                     1073

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<210> SEQ ID NO 96

<211> LENGTH: 209

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 96

-continued

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5					10					15
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
				20					25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
				35					40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
				50					55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
				65					70					75
Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200					205					

<210> SEQ ID NO 97

<211> LENGTH: 2848

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 97

gctcaagtgc cctgccttgc cccacccagc ccagcctggc cagagccccc	50
tggaagaagg gctctcttct tgcttggcag ctggaccaag ggagccagtc	100
ttgggcgctg gagggcctgt cctgaccatg gtccttcgct ggctgtggct	150
gctttgtgtc tccgtccccc aggctctccc caaggcccag cctgcagagc	200
tgctgtgga agttccagaa aactatggcg gaaatttccc tttatacctg	250
accaagttgc cgctgccccg tgagggggct gaaggccaga tcgtgctgtc	300
aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt	350
ctggcttcct gctggtgacc agggccctgg accgagagga gcaggcagag	400
taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg	450
tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc	500
atttctctca agccatctac agagctcggc tgagccgggg taccaggcct	550
ggcatccctc tcctcttcct tgaggcttca gaccgggatg agccaggcac	600
agccaactcg gatcttcgat tccacatcct gagccaggct ccagcccagc	650
cttcccaga catgttccag ctggagcctc ggctgggggc tctggccctc	700
agccccaagg ggagcaccag ccttgaccac gccctggaga ggacctacca	750

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gctgttggtgta caggtcaagg acatgggtga ccaggcctca ggcaccagg	800
ccactgccac cgtggaagtc tccatcatag agagcacctg ggtgtcccta	850
gagcctatcc acctggcaga gaatctcaaa gtcctatacc cgcaccacat	900
ggcccaggta cactggagtg ggggtgatgt gcactatcac ctggagagcc	950
atccccggg accctttgaa gtgaatgcag agggaaacct ctacgtgacc	1000
agagagctgg acagagaagc ccaggctgag tacctgctcc aggtgcgggc	1050
tcagaattcc catggcgagg actatgcggc ccctctggag ctgcacgtgc	1100
tggtgatgga tgagaatgac aacgtgccta tctgccctcc ccgtgacccc	1150
acagtcagca tccctgagct cagtccacca ggtactgaag tgactagact	1200
gtcagcagag gatgcagatg ccccggtc ccccaattcc cacgttgtgt	1250
atcagctcct gagccctgag cctgaggatg gggtagaggg gagagccttc	1300
caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccactccg	1350
agcaggccag aacatcctgc ttctggtgct ggccatggac ctggcaggcg	1400
cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat	1450
atcaatgac acgcccctga gttcatcact tcccagattg ggcctataag	1500
cctccctgag gatgtggagc cgggactct ggtggccatg ctaacagcca	1550
ttgatgctga cctcgagccc gccttcgccc tcatggattt tgccattgag	1600
aggggagaca cagaagggac ttttggcctg gattgggagc cagactctgg	1650
gcatgttaga ctcagactct gcaagaacct cagttatgag gcagctccaa	1700
gtcatgaggt ggtggtggtg gtgcagagtg tggcgaagct ggtggggcca	1750
ggcccaggcc ctggagccac cgccacggtg actgtgctag tggagagagt	1800
gatgccaccc cccaagttgg accaggagag ctacgaggcc agtgtcccca	1850
tcagtgcccc agccggtctt ttcctgctga ccatccagcc ctccgacccc	1900
atcagccgaa ccctcaggtt ctccctagtc aatgactcag agggctggct	1950
ctgcattgag aaattctccg gggaggtgca caccgccag tccttgacag	2000
gcgccagcc tggggacacc tacacggtgc ttgtggaggc ccaggatata	2050
gccctgactc ttgcccctgt gccctccaa tacctctgca cccccgcca	2100
agaccatggc ttgatcgtga gtggaccag caaggacccc gatctggcca	2150
gtgggcacgg tccctacagc ttcaccttg gtcccaaccc cacggtgcaa	2200
cgggattggc gcctccagac tctcaatggt tccatgcct acctacctt	2250
ggcctgcat tgggtggagc cacgtgaaca cataatccc gtggtggtca	2300
gccacaatgc ccagatgtg cagctcctgg ttcgagtgat cgtgtgtcgc	2350
tgcaacgtgg aggggcagt catgcgcaag gtgggccgca tgaaggcat	2400
gccacgaag ctgtcggcag tgggcacct tgtaggcacc ctggtagcaa	2450
taggaatctt cctcatcctc attttcaccc actggacat gtcaaggaa	2500
aaggacccg atcaaccagc agacagcgtg cccctgaagg cgactgtctg	2550
aatggccag gcagctctag ctgggagctt ggcctctggc tccatctgag	2600
tccctggga gagagccag caccacagat ccagcagggg acaggacaga	2650
gtagaagccc ctccatctgc cctggggtgg aggcaccatc accatcacca	2700

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ggcatgtctg cagagcctgg acaccaactt tatggactgc ccatgggagt	2750
gctccaaatg tcaggggtgtt tgcccaataa taaagcccca gagaactggg	2800
ctggggcccta tgggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaag	2848

<210> SEQ ID NO 98

<211> LENGTH: 807

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 98

Met Val Pro Ala Trp	Leu Trp Leu Leu Cys Val Ser Val Pro Gln
1	15
Ala Leu Pro Lys Ala	Gln Pro Ala Glu Leu Ser Val Glu Val Pro
20	30
Glu Asn Tyr Gly Gly	Asn Phe Pro Leu Tyr Leu Thr Lys Leu Pro
35	45
Leu Pro Arg Glu Gly	Ala Glu Gly Gln Ile Val Leu Ser Gly Asp
50	60
Ser Gly Lys Ala Thr	Glu Gly Pro Phe Ala Met Asp Pro Asp Ser
65	75
Gly Phe Leu Leu Val	Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala
80	90
Glu Tyr Gln Leu Gln	Val Thr Leu Glu Met Gln Asp Gly His Val
95	105
Leu Trp Gly Pro Gln	Pro Val Leu Val His Val Lys Asp Glu Asn
110	120
Asp Gln Val Pro His	Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu
125	135
Ser Arg Gly Thr Arg	Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala
140	150
Ser Asp Arg Asp Glu	Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe
155	165
His Ile Leu Ser Gln	Ala Pro Ala Gln Pro Ser Pro Asp Met Phe
170	180
Gln Leu Glu Pro Arg	Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly
185	195
Ser Thr Ser Leu Asp	His Ala Leu Glu Arg Thr Tyr Gln Leu Leu
200	210
Val Gln Val Lys Asp	Met Gly Asp Gln Ala Ser Gly His Gln Ala
215	225
Thr Ala Thr Val Glu	Val Ser Ile Ile Glu Ser Thr Trp Val Ser
230	240
Leu Glu Pro Ile His	Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro
245	255
His His Met Ala Gln	Val His Trp Ser Gly Gly Asp Val His Tyr
260	270
His Leu Glu Ser His	Pro Pro Gly Pro Phe Glu Val Asn Ala Glu
275	285
Gly Asn Leu Tyr Val	Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala
290	300
Glu Tyr Leu Leu Gln	Val Arg Ala Gln Asn Ser His Gly Glu Asp
305	315
Tyr Ala Ala Pro Leu	Glu Leu His Val Leu Val Met Asp Glu Asn
320	330

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Asp Asn Val Pro	Ile Cys Pro Pro Arg	Asp Pro Thr Val Ser Ile
335		340 345
Pro Glu Leu Ser	Pro Pro Gly Thr Glu	Val Thr Arg Leu Ser Ala
350		355 360
Glu Asp Ala Asp	Ala Pro Gly Ser Pro	Asn Ser His Val Val Tyr
365		370 375
Gln Leu Leu Ser	Pro Glu Pro Glu Asp	Gly Val Glu Gly Arg Ala
380		385 390
Phe Gln Val Asp	Pro Thr Ser Gly Ser	Val Thr Leu Gly Val Leu
395		400 405
Pro Leu Arg Ala	Gly Gln Asn Ile Leu	Leu Leu Val Leu Ala Met
410		415 420
Asp Leu Ala Gly	Ala Glu Gly Gly Phe	Ser Ser Thr Cys Glu Val
425		430 435
Glu Val Ala Val	Thr Asp Ile Asn Asp	His Ala Pro Glu Phe Ile
440		445 450
Thr Ser Gln Ile	Gly Pro Ile Ser Leu	Pro Glu Asp Val Glu Pro
455		460 465
Gly Thr Leu Val	Ala Met Leu Thr Ala	Ile Asp Ala Asp Leu Glu
470		475 480
Pro Ala Phe Arg	Leu Met Asp Phe Ala	Ile Glu Arg Gly Asp Thr
485		490 495
Glu Gly Thr Phe	Gly Leu Asp Trp Glu	Pro Asp Ser Gly His Val
500		505 510
Arg Leu Arg Leu	Cys Lys Asn Leu Ser	Tyr Glu Ala Ala Pro Ser
515		520 525
His Glu Val Val	Val Val Val Gln Ser	Val Ala Lys Leu Val Gly
530		535 540
Pro Gly Pro Gly	Pro Gly Ala Thr Ala	Thr Val Thr Val Leu Val
545		550 555
Glu Arg Val Met	Pro Pro Pro Lys Leu	Asp Gln Glu Ser Tyr Glu
560		565 570
Ala Ser Val Pro	Ile Ser Ala Pro Ala	Gly Ser Phe Leu Leu Thr
575		580 585
Ile Gln Pro Ser	Asp Pro Ile Ser Arg	Thr Leu Arg Phe Ser Leu
590		595 600
Val Asn Asp Ser	Glu Gly Trp Leu Cys	Ile Glu Lys Phe Ser Gly
605		610 615
Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp
620		625 630
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu
635		640 645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His
650		655 660
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser
665		670 675
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val
680		685 690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr
695		700 705
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile Ile
710		715 720

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Pro	Val	Val	Val	Ser	His	Asn	Ala	Gln	Met	Trp	Gln	Leu	Leu	Val
				725					730					735
Arg	Val	Ile	Val	Cys	Arg	Cys	Asn	Val	Glu	Gly	Gln	Cys	Met	Arg
				740					745					750
Lys	Val	Gly	Arg	Met	Lys	Gly	Met	Pro	Thr	Lys	Leu	Ser	Ala	Val
				755					760					765
Gly	Ile	Leu	Val	Gly	Thr	Leu	Val	Ala	Ile	Gly	Ile	Phe	Leu	Ile
				770					775					780
Leu	Ile	Phe	Thr	His	Trp	Thr	Met	Ser	Arg	Lys	Lys	Asp	Pro	Asp
				785					790					795
Gln	Pro	Ala	Asp	Ser	Val	Pro	Leu	Lys	Ala	Thr	Val			
				800					805					

<210> SEQ ID NO 99

<211> LENGTH: 2436

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 99

ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc	50
agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgtagga	100
gaccacagct cctggaagca ccagccttta tctcttcacc ttcaagtccc	150
ctttctcaag aatcctctgt tctttgccct ctaaagtctt ggtacatcta	200
ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag	250
aaaggaaatg ttctccttat gtttggctta ctattgcatt tagaagctgc	300
aacaaattcc aatgagacta gcacctctgc caacactgga tccagtgtga	350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc	400
agtgggttca gcacagccac catctcaggg tccagcgtga cctccaatgg	450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca	500
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata	550
gccaccaact ctgagtcag cacaacctcc agtggggcca gcacagccac	600
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact	650
ctgggtccag tgtgacctcc agtggagcca gcaactgccac caactctgag	700
tccagcacag tgtccagtag ggccagcact gccaccaact ctgagtctag	750
cacactctcc agtggggcca gcacagccac caactctgac tccagcaca	800
cctccagtgg ggctagcaca gccaccaact ctgagtccag cacaacctcc	850
agtggggcca gcacagccac caactctgag tccagcacag tgtccagtag	900
ggccagcact gccaccaact ctgagtcag cacaacctcc agtggggcca	950
gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca	1000
gccaccaact ctgagtcag cagcaacctcc agtggggcca gcacagccac	1050
caactctgac tccagcacag tgtccagtgg ggccagcact gccaccaact	1100
ctgagtccag cagcaacctcc agtggggcca gcacagccac caactctgag	1150
tccagcacga cctccagtgg ggctagcaca gccaccaact ctgactccag	1200
cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag	1250
tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc	1300
agtggggcca acacagccac caactctgag tccagtacga cctccagtgg	1350

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ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca      1400
gcactgccac caactctgag tccagcacaa cctccagtgg ggtcagcaca      1450
gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac      1500
caactctgac tccagcacaa cctccagtga ggccagcaca gccaccaact      1550
ctgagtctag cacagtgtcc agtgggatca gcacagtcac caattctgag      1600
tccagcacaa cctccagtgg ggccaacaca gccaccaact ctgggtccag      1650
tgtgacctct gcaggctctg gaacagcagc tctgactgga atgcacacaa      1700
cttcccatag tgcattctact gcagtgagtg agggcaaagcc tgggtgggtcc      1750
ctggtgcccgt gggaaatctt cctcatcacc ctggtctcgg ttgtggcggc      1800
cgtggggctc tttgctgggc tcttcttctg tgtgagaaac agcctgtccc      1850
tgagaaacac cttaaacaca gctgtctacc accctcatgg cctcaaccat      1900
ggccttggtc caggccctgg agggaaatcat ggagccccc acaggcccag      1950
gtggagtcct aactggttct ggaggagacc agtatcatcg atagccatgg      2000
agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc      2050
gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt      2100
cattcatccc aggagacccc tcccagcttt gtttgagatc ctgaaaatct      2150
tgaagaaggt attcctcacc tttcttgctt ttaccagaca ctggaaagag      2200
aatactatat tgctcattta gctaagaaat aaatacatct catctaacac      2250
acacgacaaa gagaagctgt gcttgccccg gggtggttat ctgactctga      2300
gatgaactca gttataggag aaaacctcca tgctggactc catctggcat      2350
tcaaaatctc cacagtaaaa tccaagacc tcaaaaaaaaa aaaaaaaaaa      2400
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa      2436

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<210> SEQ ID NO 100

<211> LENGTH: 596

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 100

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Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
  1             5             10            15
Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
             20             25            30
Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
             35             40            45
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
             50             55            60
Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
             65             70            75
Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
             80             85            90
Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
             95            100           105
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
            110            115           120
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
            125            130           135

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Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala	140	145	150
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	155	160	165
Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala	170	175	180
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	185	190	195
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	200	205	210
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala	215	220	225
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	230	235	240
Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala	245	250	255
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	260	265	270
Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	275	280	285
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	290	295	300
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	305	310	315
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala	320	325	330
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	335	340	345
Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala	350	355	360
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515	520	525

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Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn
 530 535 540

Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly
 545 550 555

Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro
 560 565 570

Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile
 575 580 585

Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro
 590 595

<210> SEQ ID NO 101

<211> LENGTH: 1728

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 101

ggcgcgacgc ctccgcgtta cgggatgaat taacggcggg ttccgcacgg	50
aggttgtgac ccctacggag ccccgacttg cccacgcacc ccactcggcg	100
tcgcgcggcg tgccctgctt gtcacagggt ggaggctgga actatcaggc	150
tgaaaaacag agtgggtact ctcttctggg aagctggcaa caaatggatg	200
atgtgatata tgcattccag gggaagggaa attgtggtgc ttctgaaccc	250
atggtcaatt aacgaggcag tttctagcta ctgcacgtac ttcataaagc	300
aggactctaa aagcttttga atcatgggtg catggaaagg gatttacttt	350
atactgactc tgttttggg aagctttttt ggaagcattt tcatgctgag	400
tcccttttta cctttgatgt ttgtaaacc atcttggtat cgctggatca	450
acaaccgcct tgtggcaaca tggctcacc tacctgtggc attattggag	500
accatgtttg gtgtaaaagt gattataact ggggatgcat ttgttccttg	550
agaaagaagt gtcattatca tgaaccatcg gacaagaatg gactggatgt	600
tcctgtggaa ttgcctgatg cgatatagct acctcagatt ggagaaaatt	650
tgctctaaag cgagtctcaa aggtgttcct ggatttggtt gggccatgca	700
ggctgctgcc tatatcttca ttcataaggaa atggaaggat gacaagagcc	750
atttcgaaga catgattgat tacttttgtg atattcacga accacttcaa	800
ctcctcatat tcccagaagg gactgatctc acagaaaaca gcaagtctcg	850
aagtaatgca ttgtctgaaa aaaatggact tcagaaatat gaatatgttt	900
tacatccaag aactacaggc ttacttttg tggtagaccg tctaagagaa	950
ggtaagaacc ttgatgctgt ccatgatatc actgtggcgt atcctcacia	1000
cattcctcaa tcagagaagc acctcctcca aggagacttt ccaggggaaa	1050
tccactttca cgtccaccgg tatccaatag acaccctccc cacatccaag	1100
gaggacottc aactctgggt ccacaaacgg tgggaagaga aagaagagag	1150
gctgcgttcc ttctatcaag gggagaagaa tttttatttt accggacaga	1200
gtgtcattcc accttgcaag tctgaactca gggtccttgt ggtcaaatg	1250
ctctctatac tgtattggac cctgttcagc cctgcaatgt gcctactcat	1300
atatttgtac agtcttggtt agtggtatat tataatcacc attgtaatct	1350
ttgtgctgca agagagaata ttggtggac tggagatcat agaacttgca	1400

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tggtaccgac ttttacacaa acagccacat ttaaattcaa agaaaaatga	1450
gtaagattat aaggtttgcc atgtgaaaac ctagagcata ttttggaat	1500
gttctaaacc tttctaagct cagatgcatt tttgcatgac tatgtcgaat	1550
atttcttact gccatcatta ttgtttaaag atattttgca cttaattttg	1600
tgggaaaaat attgctacaa ttttttttaa tctctgaatg taatttcgat	1650
actgtgtaca tagcaggag tagtcgggt gaaataactt gggccagaat	1700
attattaaac aatcatcagg cttttaaa	1728

<210> SEQ ID NO 102

<211> LENGTH: 414

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 102

Met His Ser Arg Gly Arg Glu Ile Val Val Leu Leu Asn Pro Trp	
1 5 10 15	
Ser Ile Asn Glu Ala Val Ser Ser Tyr Cys Thr Tyr Phe Ile Lys	
20 25 30	
Gln Asp Ser Lys Ser Phe Gly Ile Met Val Ser Trp Lys Gly Ile	
35 40 45	
Tyr Phe Ile Leu Thr Leu Phe Trp Gly Ser Phe Phe Gly Ser Ile	
50 55 60	
Phe Met Leu Ser Pro Phe Leu Pro Leu Met Phe Val Asn Pro Ser	
65 70 75	
Trp Tyr Arg Trp Ile Asn Asn Arg Leu Val Ala Thr Trp Leu Thr	
80 85 90	
Leu Pro Val Ala Leu Leu Glu Thr Met Phe Gly Val Lys Val Ile	
95 100 105	
Ile Thr Gly Asp Ala Phe Val Pro Gly Glu Arg Ser Val Ile Ile	
110 115 120	
Met Asn His Arg Thr Arg Met Asp Trp Met Phe Leu Trp Asn Cys	
125 130 135	
Leu Met Arg Tyr Ser Tyr Leu Arg Leu Glu Lys Ile Cys Leu Lys	
140 145 150	
Ala Ser Leu Lys Gly Val Pro Gly Phe Gly Trp Ala Met Gln Ala	
155 160 165	
Ala Ala Tyr Ile Phe Ile His Arg Lys Trp Lys Asp Asp Lys Ser	
170 175 180	
His Phe Glu Asp Met Ile Asp Tyr Phe Cys Asp Ile His Glu Pro	
185 190 195	
Leu Gln Leu Leu Ile Phe Pro Glu Gly Thr Asp Leu Thr Glu Asn	
200 205 210	
Ser Lys Ser Arg Ser Asn Ala Phe Ala Glu Lys Asn Gly Leu Gln	
215 220 225	
Lys Tyr Glu Tyr Val Leu His Pro Arg Thr Thr Gly Phe Thr Phe	
230 235 240	
Val Val Asp Arg Leu Arg Glu Gly Lys Asn Leu Asp Ala Val His	
245 250 255	
Asp Ile Thr Val Ala Tyr Pro His Asn Ile Pro Gln Ser Glu Lys	
260 265 270	
His Leu Leu Gln Gly Asp Phe Pro Arg Glu Ile His Phe His Val	
275 280 285	

[illegible]

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<210> SEQ ID NO 103
<211> LENGTH: 2403
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien
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<400> SEQUENCE: 103

cggtctgagc	ggctcgagtg	aagagcctct	ccacggctcc	tgcgctgag	50
acagctggcc	tgacctccaa	atcatccatc	caccctgct	gtcatctgtt	100
ttcatagtgt	gagatcaacc	cacaggaata	tccatggctt	ttgtgtctcat	150
tttggttctc	agtttctacg	agctgggtgc	aggacagtgg	caagtcactg	200
gaccggggcaa	gtttgtccag	gccttgggtg	gggaggacgc	cgtgttctcc	250
tgctccctct	ttcctgagac	cagtgcagag	gctatggaag	tgcggttctt	300
caggaatcag	ttccatgctg	tggtccacct	ctacagagat	ggggaagact	350
gggaatctaa	gcagatgcca	cagtatcgag	ggagaactga	gtttgtgaag	400
gactccattg	caggggggcg	tgctctctcta	aggctaaaa	acatcactcc	450
ctcggacatc	ggcctgtatg	ggtgctggtt	cagttcccag	atttacgatg	500
aggaggccac	ctgggagctg	cgggtggcag	cactgggctc	acttcctctc	550
atttccatcg	tgggatatgt	tgacggagggt	atccagttac	tctgctgtgc	600
ctcaggctgg	ttcccccgac	ccacagccaa	gtggaaaggt	ccacaaggac	650
aggatttgtc	ttcagactcc	agagcaaatg	cagatgggta	cagcctgtat	700
gatgtggaga	tctccattat	agtcccaggaa	aatgctggga	gcataattgtg	750
ttccatccac	cttgctgagc	agagtcatga	ggtggaatcc	aaggtattga	800
taggagagac	gtttttccag	ccctcacctt	ggcgctgggc	ttctatttta	850
ctcgggttac	tctgtggtgc	cctgtgtggt	gttgtcatgg	ggatgataat	900
tgttttcttc	aaatccaaag	ggaaaaatcca	ggcggaaactg	gactggagaa	950
gaaagcacgg	acaggcagaa	ttgagagacg	cccggaatca	cgcagtgag	1000
gtgactctgg	atccagagac	ggctcaccgc	aagctctgcg	tttctgatct	1050
gaaaactgta	acccatagaa	aagctcccca	ggaggtgcct	cactctgaga	1100

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agagatttac aaggaagagt gtggtggcctt ctcagggttt ccaagcagg	1150
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg	1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc	1250
ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc	1300
acattcaatc cccattttat cagcctcccc cccagcacc ctcctacacg	1350
agtaggggtc ttcctggact atgaggggtg gaccatctcc ttcttcaata	1400
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc	1450
ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac	1500
tcccataatc atatgtccag tgtcctgggg atgagacaga gaagaccctg	1550
cttaaagggc cccacaccac agaccacagc acagccaagg gagagtgtc	1600
ccgacagggtg gccccagctt cctctccgga gcctgcgcac agagagtcac	1650
gcccccaact ctccttttagg gagctgaggt tcttctgccc tgagccctgc	1700
agcagcgga gtcacagctt ccagatgagg ggggattggc ctgaccctgt	1750
gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca	1800
ttaggtttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt	1850
cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc	1900
tcacagggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt	1950
tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc	2000
accataaact ctgtttgctt attccacatt aatttacttt tctctatacc	2050
aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga	2100
ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct	2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag	2200
gtccatatcc ctcattaaca cagacacaaa aattctaata aaaatttta	2250
caaaattaaac taaacaatat atttaaagat gatataaac tactcagtgt	2300
ggtttgtccc acaaatgcag agttgggtta atatttaaat atcaaccagt	2350
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa	2400
aaa	2403

<210> SEQ ID NO 104

<211> LENGTH: 466

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 104

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
1				5					10					15
Ser	Gly	Gln	Trp	Gln	Val	Thr	Gly	Pro	Gly	Lys	Phe	Val	Gln	Ala
				20					25					30
Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
				35					40					45
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90

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Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr	95	100	105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile	110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly	125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile	140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg	170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile	185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu	200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu	215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu	230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile	245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys	290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro	305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val	320	325	330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val	335	340	345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp	350	355	360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn	365	370	375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr	380	385	390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr	395	400	405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe	410	415	420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys	425	430	435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr	440	445	450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp	455	460	465

Gly

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<210> SEQ ID NO 105
 <211> LENGTH: 2103
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 105

ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg	50
tggtgagggc taggaaaaga gtttgttggg aaccttggtt tatcggcctc	100
gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt	150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat	200
tgtcatttac aactgacaaa ctatatgtcg agtttggcag agaggcttct	250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc	300
attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca	350
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt	400
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact	450
tgttttacat gaaaagctgc aagatgctgt aggacccctt aaagtagatc	500
ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat	550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct	600
caggatcgtt ggtgggacag aagtagaaga gggatgaatg ccctggcagg	650
ctagcctgca gtgggatggg agtcacgctg gtggagcaac cttaattaat	700
gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc	750
tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga	800
aacgggggtct ccggagaata attgtccatg aaaaaataca acacccatca	850
catgactatg atattttctt tgcagagctt tctagccctg ttccctacac	900
aaatgcagta catagagttt gtctccctga tgcacccat gagtttcaac	950
cagggtgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatgg	1000
tacagctaaa atcatcttcg acaagcacag gtgactctca tagacgctac	1050
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt	1100
tatgtgctgg ctcccttagaa ggaataacag atgcatgcca gggtagctct	1150
ggaggaccac tggttagtgc agatgctaga gatatctggt accttgctgg	1200
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtgtt	1250
atactagagt tacggccttg cgggactgga ttacttcaaa aactggatc	1300
taagagacaa aagcctcatg gaacagataa catttttttt tgttttttgg	1350
gtgtggaggc catttttaga gatacagaat tggagaagac ttgcaaaaca	1400
gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc	1450
ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc	1500
tgcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata	1550
atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt	1600
cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga	1650
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc	1700
attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa	1750
ttccctacat ttatttggca cagaaaagta ttaggtgttt ttcttagtgg	1800

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aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag      1850
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag      1900
tccagaaaga agccaagata tatkcttatt ttcatttcca aacaactact      1950
atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata      2000
caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat      2050
ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac      2100
cca                                                            2103

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<210> SEQ ID NO 106
<211> LENGTH: 423
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 106

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Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
 1          5          10          15

Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20          25          30

Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35          40          45

Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50          55          60

Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65          70          75

Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80          85          90

Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95          100         105

Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110         115         120

Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125         130         135

Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140         145         150

Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155         160         165

Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170         175         180

Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185         190         195

Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200         205         210

Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
215         220         225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
230         235         240

Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
245         250         255

Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
260         265         270

His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
275         280         285

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Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410					415					420

Thr Gly Ile

<210> SEQ ID NO 107
 <211> LENGTH: 2397
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 107

agagaaagaa gcgtctccag ctgaagccaa tgcagccctc cggtctctccg	50
cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatc	100
cccaggcggg cgtggggcac cgggcccagc gccgacgac gctgccgttt	150
tgcccttggt agtaggatgt ggtgaaagga tggggcttct cccttacggg	200
gtcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct	250
acgccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt	300
tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga	350
aacgagggta gaggaagcag tcattttgac ttactttcct gtggttcac	400
cggatcatgat tgcgtgttgc tgtttcctta tcattgtggg gatgtagga	450
tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtacttttg	500
aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttgacat	550
atgaacagga acttatggtt ccagtacaat ggtagatat ggtcactttg	600
aaagccagga tgacaaatta tggattacct agatatcggg ggcttactca	650
tgcttggaat ttttttcaga gagagtttaa gtgctgtgga gtagtatatt	700
tcactgactg gttggaatg acagagatgg actggccccc agattcctgc	750
tgtgttagag aattcccagg atgttccaaa caggcccacc aggaagatct	800
cagtgcacct tatcaagagg gttgtgggaa gaaaatgtat tcctttttga	850
gaggaaccaa acaactgcag gtgctgaggt ttctgggaat ctccattggg	900
gtgacacaaa tcctggccat gattctcacc attactctgc tctgggctct	950
gtattatgat agaagggagc ctgggacaga ccaaatgatg tccttgaaga	1000
atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca	1050

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agcctgtcaa gaatctttga acacacatcc atggcaaaca gctttaatac      1100
acactttgag atggaggagt tataaaaaga aatgtcacag aagaaaacca      1150
caaaactgtt ttattggact tgtgaatfff tgagtacata ctatgtgttt      1200
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata      1250
tactattcta tgctttaaaa tgaggatgga aaagtttcat gtcataagtc      1300
accacctgga caataattga tgcccttaaa atgctgaaga cagatgtcat      1350
accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg      1400
aggcagcatg gtttgattag catttccgca tccatgcaa cgagtcacat      1450
atggtgggac tggagccata gtaaagggtg atttacttct accaactagt      1500
atataaagta ctaattaaat gctaacatag gaagttagaa aatactaata      1550
acttttatta ctacagcgtc tattcttctg atgctaaata aattatatat      1600
cagaaaaactt tcaatatattg tgactaccta aatgtgattt ttgctggtta      1650
ctaaaatatt cttaccactt aaaagagcaa gctaacacat tgtcttaagc      1700
tgatcagggg ttttttgtat ataagtctgt gttaaatctg tataattcag      1750
tcgatttcag ttctgataat gttagaata accattatga aaagggaaat      1800
ttgtcctgta tagcatcatt atttttagcc tttcctgtta ataaagcttt      1850
actattctgt cctgggctta tattacacat ataactgtta tttaaatact      1900
taaccactaa ttttgaaaat taccagtgtg atacatagga atcattattc      1950
agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa      2000
cttagtgtat tcagaaagga cttgtatgct gtttttctcc caaatgaaga      2050
ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca      2100
aacaagaagc aatagtctcc aagtcaatat aaattctaca gaaaatagtg      2150
ttctttttct ccagaaaaat gcttggtgaga atcattaaaa catgtgacaa      2200
tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta      2250
cacagattat taaatttttt tacaagagta tagtatatft atttgaaatg      2300
ggaaaagtgc attttactgt attttggtga ttttgtttat ttctcagaat      2350
atggaaagaa aattaaaaatg tgtcaataaa tattttctag agagtaa      2397

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<210> SEQ ID NO 108

<211> LENGTH: 305

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 108

```

Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
  1             5             10             15
Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
             20             25             30
Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
             35             40             45
Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
             50             55             60
Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
             65             70             75
Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
             80             85             90

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-continued

Leu Leu Leu Ala Trp Tyr Phe Gly Ser	Leu Leu Val Ile Phe Cys
95	100 105
Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met	
110	115 120
Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met	
125	130 135
Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp	
140	145 150
Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe	
155	160 165
Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser	
170	175 180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln	
185	190 195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met	
200	205 210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe	
215	220 225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu	
230	235 240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro	
245	250 255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His	
260	265 270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg	
275	280 285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe	
290	295 300
Glu Met Glu Glu Leu	
305	

<210> SEQ ID NO 109

<211> LENGTH: 2339

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 109

ccaaggccag agctgtggac accttatccc actcatcctc atcctcttcc	50
tctgataaag cccctaccag tgctgataaa gtctttctcg tgagagccta	100
gaggccttaa aaaaaaagt gcttgaaaga gaaggggaca aaggaacacc	150
agtattaaga ggattttcca gtgtttctgg cagttggtcc agaaggatgc	200
ctccattcct gcttctcacc tgcctcttca tcacaggcac ctccgtgtca	250
cccgtggccc tagatccttg ttctgcttac atcagcctga atgagccctg	300
gaggaaact gaccaccagt tggatgagtc tcaaggtcct cctctatgtg	350
acaacctagt gaatggggag tggtagcact tcacgggcat ggcgggagat	400
gccatgccta ctttctgcat accagaaaac cactgtggaa cccacgcacc	450
tgtctggctc aatggcagcc accccctaga aggcgacggc attgtgcaac	500
gccaggcttg tgccagcttc aatgggaact gctgtctctg gaacaccacg	550
gtggaagtca aggcttgccc tggaggctac tatgtgtatc gtctgaccaa	600
gcccagcgtc tgcttccacg tctactgtgg tcatttttat gacatctgcg	650

-continued

acgaggactg ccatggcagc tgctcagata ccagcgagtg cacatgcgct	700
ccaggaaactg tgctaggccc tgacaggcag acatgctttg atgaaaatga	750
atgtgagcaa aacaacgggtg gctgcagtga gatctgtgtg aacctcaaaa	800
actcctaccg ctgtgagtggt ggggttgccc gtgtgctaag aagtgatggc	850
aagacttggtg aagacgttga aggatgccac aataacaatg gtggctgcag	900
ccactcttgc cttggatctg agaaaggcta ccagtgtgaa tgtccccggg	950
gcctggtgct gtctgaggat aaccacactt gccaaagtcct tgtgttgtgc	1000
aaatcaaagt ccattgaagt gaacatcccc agggagctgg ttggtggcct	1050
ggagctcttc ctgaccaaca cctcctgccg aggagtgtcc aacggcacc	1100
atgtcaacat cctcttctct ctcaagacat gtggtacagt ggtcgatgtg	1150
gtgaatgaca agattgtggc cagcaacctc gtgacaggtc taccgaagca	1200
gacccccggg agcagcggg acttcatcat ccgaaccagc aagctgctga	1250
tcccggtgac ctgagagttt ccacgcctgt acaccatttc tgaaggatac	1300
gttcccaacc ttcgaaactc cccactggaa atcatgagcc gaaatcatgg	1350
gatcttccca ttcactctgg agatcttcaa ggacaatgag tttgaagagc	1400
cttaccggga agctctgccc accctcaagc ttcgtgactc cctctacttt	1450
ggcattgagc ccgtggtgca cgtgagcggc ttggaagct tggaggagag	1500
ctgctttgcc accccacct ccaagatcga cgaggtcctg aaatactacc	1550
tcacccggga tggctgtgtt tcagatgact cggtaaagca gtacacatcc	1600
cgggatcacc tagcaaagca cttccaggtc cctgtcttca agtttgtggg	1650
caaagaccac aaggaagtgt ttctgcaactg ccgggttctt gtctgtggag	1700
tgttgagca gcgttcccgc tgtgccagg gttgccaccg gcgaatgcgt	1750
cgtggggcag gaggagagga ctcagccggt ctacagggcc agacgctaac	1800
aggcggcccc atccgcatcg actgggagga ctagtctgta gccatacctc	1850
gagtcctgc attggacggc tctgtctttt ggagcttctc cccccaccgc	1900
cctctaagaa catctgccaa cagctgggtt cagacttcac actgtgagtt	1950
cagactccca gcaccaactc actctgattc tggtecatte agtgggcaca	2000
ggtcacagca ctgctgaaca atgtggcctg ggtggggttt catctttcta	2050
gggttgaaaa ctaaactgtc caccagaaa gacactcacc ccatttccct	2100
catttctttc ctacacttaa atacctcgtg tatggtgcaa tcagaccaca	2150
aaatcagaag ctgggtataa tatttcaagt tacaaccct agaaaaatta	2200
aacagttact gaaattatga cttaaatacc caatgactcc ttaaatatgt	2250
aaattatagt tataccttga aatttcaatt caaatgcaga ctaattatag	2300
ggaatttgga agtgtatcaa taaaacagta tataatttt	2339

<210> SEQ ID NO 110

<211> LENGTH: 545

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 110

Met	Pro	Pro	Phe	Leu	Leu	Leu	Thr	Cys	Leu	Phe	Ile	Thr	Gly	Thr
1				5					10					15

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Ser Val Ser Pro Val Ala Leu Asp Pro Cys Ser Ala Tyr Ile Ser	20	25	30
Leu Asn Glu Pro Trp Arg Asn Thr Asp His Gln Leu Asp Glu Ser	35	40	45
Gln Gly Pro Pro Leu Cys Asp Asn His Val Asn Gly Glu Trp Tyr	50	55	60
His Phe Thr Gly Met Ala Gly Asp Ala Met Pro Thr Phe Cys Ile	65	70	75
Pro Glu Asn His Cys Gly Thr His Ala Pro Val Trp Leu Asn Gly	80	85	90
Ser His Pro Leu Glu Gly Asp Gly Ile Val Gln Arg Gln Ala Cys	95	100	105
Ala Ser Phe Asn Gly Asn Cys Cys Leu Trp Asn Thr Thr Val Glu	110	115	120
Val Lys Ala Cys Pro Gly Gly Tyr Tyr Val Tyr Arg Leu Thr Lys	125	130	135
Pro Ser Val Cys Phe His Val Tyr Cys Gly His Phe Tyr Asp Ile	140	145	150
Cys Asp Glu Asp Cys His Gly Ser Cys Ser Asp Thr Ser Glu Cys	155	160	165
Thr Cys Ala Pro Gly Thr Val Leu Gly Pro Asp Arg Gln Thr Cys	170	175	180
Phe Asp Glu Asn Glu Cys Glu Gln Asn Asn Gly Gly Cys Ser Glu	185	190	195
Ile Cys Val Asn Leu Lys Asn Ser Tyr Arg Cys Glu Cys Gly Val	200	205	210
Gly Arg Val Leu Arg Ser Asp Gly Lys Thr Cys Glu Asp Val Glu	215	220	225
Gly Cys His Asn Asn Asn Gly Gly Cys Ser His Ser Cys Leu Gly	230	235	240
Ser Glu Lys Gly Tyr Gln Cys Glu Cys Pro Arg Gly Leu Val Leu	245	250	255
Ser Glu Asp Asn His Thr Cys Gln Val Pro Val Leu Cys Lys Ser	260	265	270
Asn Ala Ile Glu Val Asn Ile Pro Arg Glu Leu Val Gly Gly Leu	275	280	285
Glu Leu Phe Leu Thr Asn Thr Ser Cys Arg Gly Val Ser Asn Gly	290	295	300
Thr His Val Asn Ile Leu Phe Ser Leu Lys Thr Cys Gly Thr Val	305	310	315
Val Asp Val Val Asn Asp Lys Ile Val Ala Ser Asn Leu Val Thr	320	325	330
Gly Leu Pro Lys Gln Thr Pro Gly Ser Ser Gly Asp Phe Ile Ile	335	340	345
Arg Thr Ser Lys Leu Leu Ile Pro Val Thr Cys Glu Phe Pro Arg	350	355	360
Leu Tyr Thr Ile Ser Glu Gly Tyr Val Pro Asn Leu Arg Asn Ser	365	370	375
Pro Leu Glu Ile Met Ser Arg Asn His Gly Ile Phe Pro Phe Thr	380	385	390
Leu Glu Ile Phe Lys Asp Asn Glu Phe Glu Glu Pro Tyr Arg Glu	395	400	405

-continued

Ala Leu Pro Thr Leu Lys Leu Arg Asp Ser Leu Tyr Phe Gly Ile
410 415 420

Glu Pro Val Val His Val Ser Gly Leu Glu Ser Leu Val Glu Ser
425 430 435

Cys Phe Ala Thr Pro Thr Ser Lys Ile Asp Glu Val Leu Lys Tyr
440 445 450

Tyr Leu Ile Arg Asp Gly Cys Val Ser Asp Asp Ser Val Lys Gln
455 460 465

Tyr Thr Ser Arg Asp His Leu Ala Lys His Phe Gln Val Pro Val
470 475 480

Phe Lys Phe Val Gly Lys Asp His Lys Glu Val Phe Leu His Cys
485 490 495

Arg Val Leu Val Cys Gly Val Leu Asp Glu Arg Ser Arg Cys Ala
500 505 510

Gln Gly Cys His Arg Arg Met Arg Arg Gly Ala Gly Gly Glu Asp
515 520 525

Ser Ala Gly Leu Gln Gly Gln Thr Leu Thr Gly Gly Pro Ile Arg
530 535 540

Ile Asp Trp Glu Asp
545

<210> SEQ ID NO 111

<211> LENGTH: 2063

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 111

gagagaggca gcagcttgct cagcggacaa ggatgctggg cgtgagggac	50
caaggcctgc cctgcactcg ggccctcctcc agccagtgtc gaccagggac	100
ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctctgtctgc	150
cttgggggtga caatctcagc tccaggctac agggagaccg ggaggatcac	200
agagccagca tggtacagga tcctgacagt gatcaacctc tgaacagcct	250
cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa	300
aggtggggat ccccatcatc atagcactac tgagcctggc gagtatcatc	350
attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg	400
cgggcagcct ctccacttca tcccaggaa gcagctgtgt gacggagagc	450
tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc	500
gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca	550
ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttcgacaact	600
tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga	650
gctgtggaga ttggcccaga ccaggatctg gatgtgttg aaatcacaga	700
aaacagccag gagcttcgca tgcggaactc aagtggggccc tgtctctcag	750
gctccctggt ctccctgcac tgtcttgctt gtgggaagag cctgaagacc	800
ccccgtgtgg tgggtgggga ggaggcctct gtggattctt ggccttggca	850
ggtcagcatc cagtacgaca aacagcacgt ctgtggaggg agcatcctgg	900
acccccactg ggtcctcacg gcagccact gcttcaggaa acataccgat	950
gtgttcaact ggaaggtgcg gccaggctca gacaaactgg gcagcttccc	1000
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc	1050

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ccaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcactttc      1100
tcaggcacag tcaggcccat ctgtctgccc ttctttgatg aggagctcac      1150
tccagccacc ccactctgga tcattggatg gggctttacg aagcagaatg      1200
gaggggaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac      1250
agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa      1300
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg      1350
acagtgtgtg gcccctgatg taccaatctg accagtggca tgtggtgggc      1400
atcgttagct ggggctatgg ctgctggggc cagagcagcc caggagtata      1450
caccaagggtc tcagcctatc tcaactggat ctacaatgtc tggaaggctg      1500
agctgtaatg ctgctgcccc ttgtcagtgc tgggagccgc ttccttctctg      1550
ccctgcccac ctgggggatcc cccaaagtca gacacagagc aagagtcccc      1600
ttgggtacac ccctctgccc acagcctcag catttcttgg agcagcaaag      1650
ggcctcaatt cctgtaagag accctcgagc cccagaggcg cccagaggaa      1700
gtcagcagcc ctgctcggc cactctggtg gctcccagca tcccagggag      1750
agacacagcc cactgaacaa ggtctcaggg gtattgctaa gccaagaagg      1800
aactttccca cactactgaa tggaagcagg ctgtcttcta aaagcccaga      1850
tactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg      1900
tcttcacca tcccaagcc tactagagca agaaccagt tgtaatatata      1950
aatgcactgc cctactgttg gtatgactac cgttacctac tgttgtcatt      2000
gttattacag ctatggccac tattattaaa gagctgtgta acatctcttg      2050
caaaaaaaaa aaa                                              2063

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<210> SEQ ID NO 112

<211> LENGTH: 432

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 112

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Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
 1             5             10            15
Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
 20            25            30
Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
 35            40            45
Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
 50            55            60
Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
 65            70            75
Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
 80            85            90
His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
 95           100           105
Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110           115           120
Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125           130           135
Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu

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	140		145		150
Ile Gly Pro Asp	Gln Asp Leu Asp Val	Val Glu Ile Thr Glu Asn			
	155	160	165		
Ser Gln Glu Leu Arg	Met Arg Asn Ser	Ser Gly Pro Cys Leu Ser			
	170	175	180		
Gly Ser Leu Val Ser	Leu His Cys Leu	Ala Cys Gly Lys Ser Leu			
	185	190	195		
Lys Thr Pro Arg Val	Val Gly Gly Glu	Glu Ala Ser Val Asp Ser			
	200	205	210		
Trp Pro Trp Gln Val	Ser Ile Gln Tyr	Asp Lys Gln His Val Cys			
	215	220	225		
Gly Gly Ser Ile Leu	Asp Pro His Trp	Val Leu Thr Ala Ala His			
	230	235	240		
Cys Phe Arg Lys His	Thr Asp Val Phe	Asn Trp Lys Val Arg Ala			
	245	250	255		
Gly Ser Asp Lys Leu	Gly Ser Phe Pro	Ser Leu Ala Val Ala Lys			
	260	265	270		
Ile Ile Ile Ile Glu	Phe Asn Pro Met	Tyr Pro Lys Asp Asn Asp			
	275	280	285		
Ile Ala Leu Met Lys	Leu Gln Phe Pro	Leu Thr Phe Ser Gly Thr			
	290	295	300		
Val Arg Pro Ile Cys	Leu Pro Phe Phe	Asp Glu Glu Leu Thr Pro			
	305	310	315		
Ala Thr Pro Leu Trp	Ile Ile Gly Trp	Gly Phe Thr Lys Gln Asn			
	320	325	330		
Gly Gly Lys Met Ser	Asp Ile Leu Leu	Gln Ala Ser Val Gln Val			
	335	340	345		
Ile Asp Ser Thr Arg	Cys Asn Ala Asp	Asp Ala Tyr Gln Gly Glu			
	350	355	360		
Val Thr Glu Lys Met	Met Cys Ala Gly	Ile Pro Glu Gly Gly Val			
	365	370	375		
Asp Thr Cys Gln Gly	Asp Ser Gly Gly	Pro Leu Met Tyr Gln Ser			
	380	385	390		
Asp Gln Trp His Val	Val Gly Ile Val	Ser Trp Gly Tyr Gly Cys			
	395	400	405		
Gly Gly Pro Ser Thr	Pro Gly Val Tyr	Thr Lys Val Ser Ala Tyr			
	410	415	420		
Leu Asn Trp Ile Tyr	Asn Val Trp Lys	Ala Glu Leu			
	425	430			

<210> SEQ ID NO 113

<211> LENGTH: 1768

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 113

ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc	50
aagggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac	100
tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac	150
tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt	200
tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca	250
ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt	300

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ttctaccac accgtccct cgaagccggg gacagcctca ccttgctggc	350
ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcaactg	400
actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg	450
tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata	500
ggcgatggct cccactgccc aggcacagc cttgctgtag tcaatcactg	550
ccctggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag	600
acatcacgct gcccggccat ctaacctttt catgtcctgc acatcacctg	650
atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga	700
gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg	750
acaggacttg cattctcctg gaacatgagg gaacgccgga ggaagcaaaa	800
gtggcagggg aggaacttgt gccaaattat gggtcagaaa agatggaggt	850
gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg	900
ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc	950
atcagacagc cgtttccgcc ccgatccagc taccagctgc tgaagggcaa	1000
ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca	1050
ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc	1100
ctccctcct tccctctgag aggcctcct atgtccctac taaagccacc	1150
agcaagacat agctgacagg ggctaattgc tcagtgttgg ccagggaggt	1200
cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa	1250
tgctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg	1300
ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaagg	1350
agctagagct tggttcaaat gatctccaag ggccttata cccagggaga	1400
ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgcat	1450
taagaatcag ttattgccg gtgtgtgtgc ctgtaatgcc aacattttgg	1500
gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg	1550
gccaacatgg tgaaccacct gtctctacta aaaatacaaa aaaactagcc	1600
aggcatgggt gtgtgtgcct gtatccagc tactcgggag gctgagacag	1650
gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac	1700
ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag	1750
aattatgggt atttgtaa	1768

<210> SEQ ID NO 114

<211> LENGTH: 109

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 114

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
1				5					10				15

Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60

-continued

Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
65 70 75

Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
80 85 90

Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
95 100 105

Arg Arg Arg Asp

<210> SEQ ID NO 115
<211> LENGTH: 1197
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 115

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cagcagtggc ctctcagtcc tctcaaagca aggaaagagt actgtgtgct      50
gagagacccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt      100
ctaaatgcag aagcttttta atccaagaaa atatgtaaat cacttaagat      150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtctgtttt      200
gggggagcaa gcacttctgg cgggaggtac ccaaaaaagc ctatgacatg      250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat      300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg      350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc      400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga      450
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa      500
ctttctttga acagtcatg atttgggtcc cagcagaaaa gcctattgaa      550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt      600
gaccatgtat tggatcaatc ccaacttaat atcagtttct gagttacaag      650
actttgagga ggaggagaa gatcttcact ttcctgcaa cgaaaaaaaaa      700
gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa      750
gacccgtcac gccagacaag caagtgagga agaacttcca ataatgact      800
atactgaaaa tggaatagaa ttgatccca tgctggatga gagaggttat      850
tgttgtatct actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga      900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag      950
tcactgtctg tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg     1000
gggaggggtc aataggaggt ttgagctcaa atgcttaaac tgctggcaac     1050
atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg     1100
ccccgtgtag ccagctctcc agaattactt gtaggtaatt cctctcttca     1150
tggttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa     1197

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<210> SEQ ID NO 116
<211> LENGTH: 317
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 116

Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu
1 5 10 15

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Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys
      20              25              30
Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
      35              40              45
Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
      50              55              60
Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
      65              70              75
Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe
      80              85              90
Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe
      95              100             105
Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys
      110             115             120
Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro
      125             130             135
Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe
      140             145             150
Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn
      155             160             165
Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn
      170             175             180
Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu
      185             190             195
Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala
      200             205             210
Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro
      215             220             225
Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
      230             235             240
Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe
      245             250             255
Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg
      260             265             270
Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
      275             280             285
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
      290             295             300
Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
      305             310             315
Arg Val

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<210> SEQ ID NO 117
<211> LENGTH: 2121
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 117

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```

gagctccct caggagcgcg ttagcttcac accttcggca gcaggagggc      50
ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac      100
cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct      150
gcacgcgggc caccgggatg gacatgtgga gcacccagga cctgtacgac      200
aaccctgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt      250

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gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg	300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc	350
gtcctgggtg ccattggcct cctggtatcc atctttgccc tgaatgcat	400
ccgcattggc agcatggagg actctgcca agccaacatg acactgacct	450
ccgggatcat gttcatgtc tcaggtcttt gtgcaattgc tggagtgtct	500
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat	550
gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat	600
ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cactactaatt	650
gggggtgtga tgatgtgcat cgcctgccgg gccctggcac cagaagaaac	700
caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca	750
agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac	800
aagaagatat acgatggagg tgcccgca gaggacgagg tacaatctta	850
tccttccaag cagcactatg tgtaatgctc taagacctct cagcagggc	900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag	950
atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt	1000
catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata	1050
ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac	1100
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga	1150
gagaatgtgg ttttaatctc tctctccat tttgatgatt tagacagact	1200
ccccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct	1250
tatccccaag aaaacttttg aaaggaaaga gtagacccta agatgttatt	1300
ttctgctgtt tgaattttgt ctcccccccc ccaacttggc tagtaataaa	1350
cacttactga agaagaagca ataagagaaa gatatttgta atctctccag	1400
cccatgatct cggttttctt acactgtgat cttaaaagtt accaaaccaa	1450
agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct	1500
tcttattaca gcaacacat tctaggagt tctgagctc tccactggag	1550
tcctctttct gtcgagggtc agaaattgtc cctagatgaa tgagaaaatt	1600
atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag	1650
taaaatgata cactatctct gtgaaatagc ctaccccta catgtggata	1700
gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt	1750
aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct	1800
agcactttgg gaggtgagg aggaaggatc acttgagccc agaagttcga	1850
gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag	1900
aaaaaatcag ccagtcattg tggcatacac ctgtagtccc agcattccgg	1950
gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt	2000
gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct	2050
gtctaaaaaa ataaaaaata aataatggaa cacagcaagt cctaggaagt	2100
aggttaaaac taattcttta a	2121

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<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 118
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
  1             5             10             15
Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20             25             30
Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35             40             45
Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50             55             60
Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65             70             75
Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly
 80             85             90
Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg
 95            100            105
Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr
110            115            120
Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly
125            130            135
Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser
140            145            150
Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val
155            160            165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val
170            175            180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala
185            190            195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser
200            205            210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe
215            220            225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
230            235            240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro
245            250            255
Ser Lys His Asp Tyr Val
260

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<210> SEQ ID NO 119
<211> LENGTH: 2010
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 119

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```

ggaaaaactg ttctcttctg tggcacagag aacctgctt caaagcagaa      50
gtagcagttc cggagtccag ctggctaaaa ctcattccag aggataatgg     100
caacccatgc cttagaaatc gctgggctgt ttcttggttg tgttggaatg     150
gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt     200
cattgaaaac aacatcgttg tttttgaaaa cttctgggaa ggactgtgga     250
tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat     300

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tccctgctgg ctcttttctcc ggacctacag gcagccagag gactgatgtg	350
tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttgga	400
tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt	450
ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tggtgctcat	500
ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa	550
tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga	600
tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgctg	650
ttttgttg caccgaaaaga gcagtagcta cagatactcg atacctccc	700
atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc	750
tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta	800
taaagccatg caaatgacaa aaatctatat tacttttctca aaatggaccc	850
caaagaaact ttgatttact gttcttaact gcctaactctt aattacagga	900
actgtgcatc agctattttat gattctataa gctattttcag cagaatgaga	950
tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc	1000
taagggtggt caagcatcta ctctttttat catttacttc aaaatgacat	1050
tgctaaagac tgcattattt tactactgta atttctccac gacatagcat	1100
tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta	1150
tatgggtttta tttaaatga aatgccagtc cattacactg aataaataga	1200
actcaactat tgcttttcag ggaaatcatg gatagggttg aagaaggtta	1250
ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat	1300
gaagattaaa atgaaggcct taatcagcat tgtaaaggaa attgaatggc	1350
tttctgatat gctgtttttt agcctaggag ttgaaatcc taacttcttt	1400
atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt	1450
ttaaaacgca gatattttgt caaggggctt tgcattcaa ctgcttttcc	1500
agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg	1550
gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat	1600
gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt	1650
gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata	1700
tgtcttggtt ttcatttgct taccaaaaaa acaacaacaa aaaaagttgt	1750
cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc	1800
atttttgttc tgtgaaaaat aaatttcctt cttgtacat ttctgtttag	1850
ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga	1900
tgaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta	1950
aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat	2000
ttttctaatt	2010

<210> SEQ ID NO 120

<211> LENGTH: 225

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 120

-continued

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	
1				5					10					15	
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	
				20					25					30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	
				35					40					45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	
				50					55					60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	
				65					70					75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	
				80					85					90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	
				95					100					105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	
				110					115					120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	
				125					130					135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	
				140					145					150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	
				155					160					165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	
				170					175					180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	
				185					190					195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	
				200					205					210	
Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val	
				215					220					225	

<210> SEQ ID NO 121

<211> LENGTH: 1257

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 121

ggagagagggc gcgcgggtga aaggcgcatg gatgcagcct gcggcggcct	50
cggagcgcg cggagccaga cgctgaccac gttcctctcc tcggtctcct	100
ccgctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg	150
gccccgcgc ctccccgcag cggctccgc gcctcctgct gctcctgctg	200
ctgcagctgc ccgcgcccgc gagcgccctc gagatcccca aggggaagca	250
aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt	300
gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc	350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg	400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca	450
actacaagca gtgttcattg agttcattga attatggcat agatcttggg	500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag	550
agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc	600
agcgttggtta ttccacattc aatggagctg aatgttcagg acctcttccc	650

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attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac      700
aattaatatt catcgcaactt cttctgtgga aggactttgt gaaggaattg      750
gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac      800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat      850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt      900
ttattatgcc ttggaatggt tcacttaaat gacattttaa ataagtttat      950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg     1000
tgatttcaca ctgtttttaa atctagcatt attcattttg cttcaatcaa     1050
aagtggtttc aatatttttt ttagttggtt agaatacttt cttcatagtc     1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt     1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac     1200
aatttgtaaa tgtaagaat tttttttata tctgttaaat aaaaattatt     1250
tccaaca                                           1257

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<210> SEQ ID NO 122

<211> LENGTH: 243

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 122

```

Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1           5           10           15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20          25          30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35          40          45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50          55          60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65          70          75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80          85          90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95         100         105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110         115         120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125         130         135
Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140         145         150
Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155         160         165
Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170         175         180
Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185         190         195
Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200         205         210
Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215         220         225

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Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> SEQ ID NO 123

<211> LENGTH: 2379

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 123

gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc	50
agctctgtgg ctgaactggg tgctcatcac gggaaactgct gggctatgga	100
atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc	150
atgttttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc	200
ccccctccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc	250
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg	300
tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaagaata	350
atgttccaaa atcgggtccat ctcccagggt gtccaatttt tcttcctggg	400
tgtcagcgag ccctgactca ctacagtgcg gctgacaggg gctgtcatgc	450
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat	500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag	550
cactggttat agccccact gtcttactga caatgccttc ttctgccgaa	600
cgaggatgcc ctaagggtcg taggtgtgaa ggcaaatgg tatattgtga	650
atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag	700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt	750
aaagggtcga accagctcac ctggctatac cttgaccata accatatcag	800
caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga	850
ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct	900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct	950
gggactctgaa cagtttcggg gcttgccgaa gctgctgagt ttacatttac	1000
ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc	1050
aacctggaac ttttgacct gggatataac cggatccgaa gtttagccag	1100
gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca	1150
atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt	1200
cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat	1250
gtcctggacc tggagctcct tacaaggct tgatttatca ggcaatgaga	1300
tcgaagcttt cagtggaccc agtgttttcc agtgtgtccc gaatctgcag	1350
cgctcaacc tggattccaa caagctcaca tttattggtc aagagatttt	1400
ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg	1450
aatgcagcag aaatatattg tcccttgtaa actggctgaa aagttttaa	1500
ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg	1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta	1600
ctacagagag gtttgatctg gccagggtcc toccaaagcc gacgtttaag	1650

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cccaagctcc ccaggccgaa gcatgagagc aaacccccctt tgcccccgac      1700
ggtgggagcc acagagcccc gccagagagc cgatgctgac gccgagcaca      1750
tctctttcca taaaatcadc gcgggcagcg tggcgctttt cctgtccgtg      1800
ctcgtcatcc tgctggttat ctacgtgtca tggaagcggt accctgcgag      1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga      1900
aaagacagtc cctaaagcaa atgactccca gcacccagga attttatgta      1950
gattataaac ccaccaaacac ggagaccagc gagatgctgc tgaatgggac      2000
gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa      2050
ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgcttta      2100
ttgaactctg gtgactatca agggaacgcy atgccccccc tccccctccc      2150
tctccctctc actttggtgg caagatcctt ccttgctcgt tttagtgcac      2200
tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt      2250
aaataccaca atcaatgtga agcttgaact cgggtttaat ataataccta      2300
ttgtataaga ccctttactg attccattaa tgcgcattt gttttaagat      2350
aaaacttctt tcataggtaa aaaaaaaaaa      2379

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<210> SEQ ID NO 124

<211> LENGTH: 513

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 124

```

Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
  1             5             10            15
Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
             20             25            30
Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
             35             40            45
Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
             50             55            60
Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
             65             70            75
Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
             80             85            90
Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
             95            100           105
Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
            110            115           120
Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
            125            130           135
Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
            140            145           150
Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
            155            160           165
Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
            170            175           180
Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
            185            190           195
Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu
            200            205           210

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His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe
 215 220 225
 Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys
 230 235 240
 Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu
 245 250 255
 Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly
 260 265 270
 Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu
 275 280 285
 Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser
 290 295 300
 Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu
 305 310 315
 Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe
 320 325 330
 Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu
 335 340 345
 Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile
 350 355 360
 Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu
 365 370 375
 Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu
 380 385 390
 Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly
 395 400 405
 Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile
 410 415 420
 Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu
 425 430 435
 Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
 440 445 450
 Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
 455 460 465
 Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
 470 475 480
 Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
 485 490 495
 Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510
 Cys Glu Val

<210> SEQ ID NO 125

<211> LENGTH: 998

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 125

ccgttatcgt cttgcgctac tgctgaatgt ccgtcccggga ggaggaggag	50
aggctttttgc cgctgaccca gagatggccc cgagcgagca aattcctact	100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc	150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg	200

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ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc	250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga	300
caccgcgcat ttacagacac gtagtgtatt ctggaggctg aatggtcaca	350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta	400
ttccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc	450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa	500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca	550
tgcatattgca aaaatccttag ctgaaggagg aatacgaggg ctttgggcag	600
gctgggtacc caatatataa agagcagcac tggatgaatat gggagattta	650
accacttatg atacagtga acactacttg gtattgaata caccacttga	700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag	750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat	800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga	850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag	900
gctttttacc atcttggctg agaatgacct cttggtcaat ggtgttctgg	950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa	998

<210> SEQ ID NO 126

<211> LENGTH: 323

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 126

Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln	
1 5 10 15	
Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala	
20 25 30	
Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr	
35 40 45	
Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp	
50 55 60	
Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala	
65 70 75	
Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly	
80 85 90	
Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg	
95 100 105	
Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser	
110 115 120	
Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met	
125 130 135	
Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu	
140 145 150	
Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly	
155 160 165	
Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile	
170 175 180	
Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro	
185 190 195	

-continued

Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr
				260					265					270
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly
				275					280					285
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met
				290					295					300
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg
				305					310					315
Glu	Met	Ser	Gly	Val	Ser	Pro	Phe							
				320										

<210> SEQ ID NO 127

<211> LENGTH: 1505

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 127

cgcgatcgg acccaagcag gtcggcggcg gcggcaggag agcggccggg	50
cgtcagctcc tcgacccccg tgcgggcta gtccagcgag gcggacgggc	100
ggcgtggggc catggccagg cccggcatgg agcgggtggcg cgaccggctg	150
gcgctggtga cgggggcctc ggggggcctc ggcgcggccg tggcccgggc	200
cctggtccag cagggaactga aggtggtggg ctgcgcccg actgtgggca	250
acatcgagga gctggctgct gaattgaaga gtgcaggcta ccccgggact	300
ttgatccct acagatgtga cctatcaaat gaagaggaca tcctctccat	350
gttctcagct atccgttctc agcacagcgg tgtagacatc tgcataaca	400
atgttggtt ggcccgccct gacaccctgc tctcaggcag caccagtgg	450
tgaagagaca tgttcaatgt gaacgtgctg gccctcagca tctgcacacg	500
ggaagcctac cagtccatga aggagcggaa tgtggacgat gggcacatca	550
taaacaatcaa tagcatgtct ggccaccgag tgttaccct gtctgtgacc	600
cacttctata gtgccaccaa gtatgccgtc actgcgctga cagagggact	650
gaggcaagag cttcgggagg ccagaccca catccgagcc acgtgcatct	700
ctccaggtgt ggtggagaca caattgcct tcaaaactcca cgacaaggac	750
cctgagaagg cagctgccac ctatgagcaa atgaagtgtc tcaaaccgca	800
ggatgtggcc gaggtgtta tctacgtcct cagcaccccc gcacacatcc	850
agattggaga catccagatg agggccacgg agcaggtgac ctagtgtactg	900
tgggagctcc tccttcctc cccacccttc atggcttgcc tcctgcctct	950
ggattttagg tgttgatttc tggatcacgg gataccactt cctgtccaca	1000
ccccgaccag gggctagaaa atttgtttga gatttttata tcattctgtc	1050
aaattgcttc agttgtaaat gtgaaaaatg ggctggggaa aggaggtgg	1100

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gtccctaatt gttttacttg ttaacttggt cttgtgcccc tgggcacttg	1150
gcctttgtct gctctcagtg tcttcctttt gacatgggaa aggagtgtg	1200
gccaaaatcc ccatcttctt gcacctcaac gtctgtggct cagggctggg	1250
gtggcagagg gaggccttca ccttatatct gtgttggtat ccagggtctc	1300
agacttcctc ctctgcctgc cccactgcac cctctcccc ttatctatct	1350
ccttctcggc tccccagccc agtcttggtt tcttgctccc tcctggggtc	1400
atccctccac tctgactctg actatggcag cagaacacca gggcctggcc	1450
cagtggattt catggtgatc attaaaaag aaaaatcgca accaaaaaaa	1500
aaaaa	1505

<210> SEQ ID NO 128

<211> LENGTH: 260

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 128

Met Ala Arg Pro Gly Met Glu Arg Trp Arg Asp Arg Leu Ala Leu	1	5	10	15
Val Thr Gly Ala Ser Gly Gly Ile Gly Ala Ala Val Ala Arg Ala	20	25	30	
Leu Val Gln Gln Gly Leu Lys Val Val Gly Cys Ala Arg Thr Val	35	40	45	
Gly Asn Ile Glu Glu Leu Ala Ala Glu Cys Lys Ser Ala Gly Tyr	50	55	60	
Pro Gly Thr Leu Ile Pro Tyr Arg Cys Asp Leu Ser Asn Glu Glu	65	70	75	
Asp Ile Leu Ser Met Phe Ser Ala Ile Arg Ser Gln His Ser Gly	80	85	90	
Val Asp Ile Cys Ile Asn Asn Ala Gly Leu Ala Arg Pro Asp Thr	95	100	105	
Leu Leu Ser Gly Ser Thr Ser Gly Trp Lys Asp Met Phe Asn Val	110	115	120	
Asn Val Leu Ala Leu Ser Ile Cys Thr Arg Glu Ala Tyr Gln Ser	125	130	135	
Met Lys Glu Arg Asn Val Asp Asp Gly His Ile Ile Asn Ile Asn	140	145	150	
Ser Met Ser Gly His Arg Val Leu Pro Leu Ser Val Thr His Phe	155	160	165	
Tyr Ser Ala Thr Lys Tyr Ala Val Thr Ala Leu Thr Glu Gly Leu	170	175	180	
Arg Gln Glu Leu Arg Glu Ala Gln Thr His Ile Arg Ala Thr Cys	185	190	195	
Ile Ser Pro Gly Val Val Glu Thr Gln Phe Ala Phe Lys Leu His	200	205	210	
Asp Lys Asp Pro Glu Lys Ala Ala Ala Thr Tyr Glu Gln Met Lys	215	220	225	
Cys Leu Lys Pro Glu Asp Val Ala Glu Ala Val Ile Tyr Val Leu	230	235	240	
Ser Thr Pro Ala His Ile Gln Ile Gly Asp Ile Gln Met Arg Pro	245	250	255	
Thr Glu Gln Val Thr				

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260

<210> SEQ ID NO 129

<211> LENGTH: 1177

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 129

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aacttctaca tgggcctcct gctgctggtg ctcttcctca gcctcctgcc      50
ggtggcctac accatcatgt ccctcccacc ctcttttgac tgcgggccgt      100
tcaggtgcag agtctcagtt gcccgggagc acctcccctc ccgaggcagt      150
ctgctcagag ggcctcggcc cagaattcca gttctggttt catgccagcc      200
tgtaaaaggc catggaactt tgggtgaatc accgatgcc a ttaagaggg      250
ttttctgcca ggatggaaat gttaggtcgt tctgtgtctg cgctgttcat      300
ttcagtagcc accagccacc tgtggccgtt gagtgcctga aatgaggaac      350
tgagaaaatt aattttctcat gtatttttct catttattta ttaattttta      400
actgatagtt gtacatatTTT ggggggtacat gtgatatttg gatacatgta      450
tacaatatat aatgatcaaa tcagggtaac tgggatatcc atcacatcaa      500
acatttattt ttattctttt ttagacagag tctcactctg taccacaggc      550
tggagtgcag tggtgccatc tcagcttact gcaacctctg cctgccaggt      600
tcaagcgatt ctcatgcctc cacctcccaa gtagctggga ctacaggcat      650
gcaccacaat gcccactaa tttttgtatt tttagtagag acggggtttt      700
gccatgttgc ccaggctggc cttgaactcc tggcctcaa caatccactt      750
gcctcggcct cccaaagtgt tatgattaca ggcgtgagcc accgtgcctg      800
gcctaaacat ttatcttttc tttgtgttgg gaactttgaa attatacaat      850
gaattattgt taactgtcat ctccctgctg tgctatggaa cactgggact      900
tcttcctctc atctaactgt atatttgta cagttaacca accgtacttc      950
atccccactc ctctctatcc ttcccaacct ctgatcacct cattctactc     1000
tctacctcca tgagatccac ttttttagct cccacatgtg agtaagaaaa     1050
tgcaatattt gtctttctgt gcctggctta tttcacttaa cataatgact     1100
tcctgttcca tccatgttgc tgcaaatgac aggatttcgt tcttaatttc     1150
aattaaaata accacacatg gcaaaaaa                                1177

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<210> SEQ ID NO 130

<211> LENGTH: 111

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 130

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Met Gly Leu Leu Leu Leu Val Leu Phe Leu Ser Leu Leu Pro Val
  1             5             10             15
Ala Tyr Thr Ile Met Ser Leu Pro Pro Ser Phe Asp Cys Gly Pro
          20             25             30
Phe Arg Cys Arg Val Ser Val Ala Arg Glu His Leu Pro Ser Arg
          35             40             45
Gly Ser Leu Leu Arg Gly Pro Arg Pro Arg Ile Pro Val Leu Val
          50             55             60
Ser Cys Gln Pro Val Lys Gly His Gly Thr Leu Gly Glu Ser Pro

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65	70	75	
Met Pro Phe Lys Arg Val Phe Cys Gln Asp Gly Asn Val Arg Ser			
80	85	90	
Phe Cys Val Cys Ala Val His Phe Ser Ser His Gln Pro Pro Val			
95	100	105	
Ala Val Glu Cys Leu Lys			
110			
 <210> SEQ ID NO 131			
<211> LENGTH: 2061			
<212> TYPE: DNA			
<213> ORGANISM: Homo Sapien			
 <400> SEQUENCE: 131			
ttctgaagta acggaagcta ccttgtataa agacctcaac actgctgacc		50	
atgatcagcg cagcctggag catcttcctc atcgggacta aaattgggct		100	
gttccttcaa gtagcacctc tatcagttat ggctaaatcc tgtccatctg		150	
tgtgtcgctg cgatgcgggt ttcatttact gtaatgatcg ctttctgaca		200	
tccattccaa caggaataacc agaggatgct acaactctct accttcagaa		250	
caaccaaata aataatgctg ggattccttc agatttgaaa aacttgctga		300	
aagtagaaag aatataccta taccacaaca gtttagatga atttcctacc		350	
aacctcccaa agtatgtaaa agagttacat ttgcaagaaa ataacataag		400	
gactatcact tatgattcac tttcaaaaat tccctatctg gaagaattac		450	
atttagatga caactctgtc tctgcagtta gcataagaaga gggagcattc		500	
cgagacagca actatctccg actgcttttc ctgtcccgtat atcaccttag		550	
cacaattccc tggggtttgc ccaggactat agaagaacta cgcttgatg		600	
ataatcgcat atccactatt tcatcaccat ctcttcaagg tctcactagt		650	
ctaaaacgcc tggttctaga tggaaacctg ttgaacaatc atggtttagg		700	
tgacaaagtt ttcttcaacc tagttaattt gacagagctg tccctgggtgc		750	
ggaattccct gactgctgca ccagtaaacc ttccaggcac aaacctgagg		800	
aagctttatc ttcaagataa ccacatcaat cgggtgcccc caaatgcttt		850	
ttcttatcta aggcagctct atcgactgga tatgtccaat aataacctaa		900	
gtaatttacc tcagggtatc tttgatgatt tggacaatat aacacaactg		950	
attcttcgca acaatccctg gtattgcggg tgcaagatga aatgggtacg		1000	
tgactgggta caatcactac ctgtgaaggc caacgtgcgt gggctcatgt		1050	
gccaaagccc agaaaagggt cgtgggatgg ctattaagga tctcaatgca		1100	
gaactgtttg attgtaagga cagtgggatt gtaagcacca ttcagataac		1150	
cactgcaata cccaacacag tgtatcctgc ccaaggacag tggccagctc		1200	
cagtgaacaa acagccagat attaagaacc ccaagctcac taaggatcaa		1250	
caaaccacag ggagtccctc aagaaaaaca attacaatta ctgtgaagtc		1300	
tgtcacctct gataccatc atatctcttg gaaacttgct ctacctatga		1350	
ctgctttgag actcagctgg cttaaaactgg gccatagccc ggcatttgga		1400	
tctataacag aaacaattgt aacaggggaa cgcagtgagt acttggtcac		1450	
agccctggag cctgattcac cctataaagt atgcatgggt cccatggaaa		1500	

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ccagcaacct ctacctatct gatgaaactc ctgtttgtat tgagactgaa      1550
actgcacccc ttcgaaatga caaccctaca accaccctca atcgagagca      1600
agagaaagaa ccttacaaaa accccaatct acctttggct gccatcattg      1650
gtggggctgt ggccttggtt accattgccc ttcttgcttt agtgtgttgg      1700
tatgttcata ggaatggatc gctcttctca aggaactgtg catatagcaa      1750
agggaggaga agaaaggatg actatgcaga agctggcact aagaaggaca      1800
actctatcct ggaaatcagg gaaacttctt ttcagatgtt accaataagc      1850
aatgaacca tctcgaagga ggagtttgta atacacacca tatttcctcc      1900
taatggaatg aatctgtaca aaaacaatca cagtgaagc agtagtaacc      1950
gaagctacag agacagtggg attccagact cagatcactc acactcatga      2000
tgctgaagga ctcacagcag acttgtgttt tgggtttttt aaacctaaag      2050
gaggtgatgg t                                             2061

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<210> SEQ ID NO 132

<211> LENGTH: 649

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 132

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Met Ile Ser Ala Ala Trp Ser Ile Phe Leu Ile Gly Thr Lys Ile
  1             5             10            15
Gly Leu Phe Leu Gln Val Ala Pro Leu Ser Val Met Ala Lys Ser
          20            25            30
Cys Pro Ser Val Cys Arg Cys Asp Ala Gly Phe Ile Tyr Cys Asn
          35            40            45
Asp Arg Phe Leu Thr Ser Ile Pro Thr Gly Ile Pro Glu Asp Ala
          50            55            60
Thr Thr Leu Tyr Leu Gln Asn Asn Gln Ile Asn Asn Ala Gly Ile
          65            70            75
Pro Ser Asp Leu Lys Asn Leu Leu Lys Val Glu Arg Ile Tyr Leu
          80            85            90
Tyr His Asn Ser Leu Asp Glu Phe Pro Thr Asn Leu Pro Lys Tyr
          95           100           105
Val Lys Glu Leu His Leu Gln Glu Asn Asn Ile Arg Thr Ile Thr
          110           115           120
Tyr Asp Ser Leu Ser Lys Ile Pro Tyr Leu Glu Glu Leu His Leu
          125           130           135
Asp Asp Asn Ser Val Ser Ala Val Ser Ile Glu Glu Gly Ala Phe
          140           145           150
Arg Asp Ser Asn Tyr Leu Arg Leu Leu Phe Leu Ser Arg Asn His
          155           160           165
Leu Ser Thr Ile Pro Trp Gly Leu Pro Arg Thr Ile Glu Glu Leu
          170           175           180
Arg Leu Asp Asp Asn Arg Ile Ser Thr Ile Ser Ser Pro Ser Leu
          185           190           195
Gln Gly Leu Thr Ser Leu Lys Arg Leu Val Leu Asp Gly Asn Leu
          200           205           210
Leu Asn Asn His Gly Leu Gly Asp Lys Val Phe Phe Asn Leu Val
          215           220           225
Asn Leu Thr Glu Leu Ser Leu Val Arg Asn Ser Leu Thr Ala Ala
          230           235           240

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Pro Val Asn Leu	Pro Gly Thr Asn Leu	Arg Lys Leu Tyr Leu Gln
245		255
Asp Asn His Ile	Asn Arg Val Pro Pro	Asn Ala Phe Ser Tyr Leu
260		270
Arg Gln Leu Tyr	Arg Leu Asp Met Ser	Asn Asn Asn Leu Ser Asn
275		285
Leu Pro Gln Gly	Ile Phe Asp Asp Leu	Asp Asn Ile Thr Gln Leu
290		300
Ile Leu Arg Asn	Asn Pro Trp Tyr Cys	Gly Cys Lys Met Lys Trp
305		315
Val Arg Asp Trp	Leu Gln Ser Leu Pro	Val Lys Val Asn Val Arg
320		330
Gly Leu Met Cys	Gln Ala Pro Glu Lys	Val Arg Gly Met Ala Ile
335		345
Lys Asp Leu Asn	Ala Glu Leu Phe Asp	Cys Lys Asp Ser Gly Ile
350		360
Val Ser Thr Ile	Gln Ile Thr Thr Ala	Ile Pro Asn Thr Val Tyr
365		375
Pro Ala Gln Gly	Gln Trp Pro Ala Pro	Val Thr Lys Gln Pro Asp
380		390
Ile Lys Asn Pro	Lys Leu Thr Lys Asp	Gln Gln Thr Thr Gly Ser
395		405
Pro Ser Arg Lys	Thr Ile Thr Ile Thr	Val Lys Ser Val Thr Ser
410		420
Asp Thr Ile His	Ile Ser Trp Lys Leu	Ala Leu Pro Met Thr Ala
425		435
Leu Arg Leu Ser	Trp Leu Lys Leu Gly	His Ser Pro Ala Phe Gly
440		450
Ser Ile Thr Glu	Thr Ile Val Thr Gly	Glu Arg Ser Glu Tyr Leu
455		465
Val Thr Ala Leu	Glu Pro Asp Ser Pro	Tyr Lys Val Cys Met Val
470		480
Pro Met Glu Thr	Ser Asn Leu Tyr Leu	Phe Asp Glu Thr Pro Val
485		495
Cys Ile Glu Thr	Glu Thr Ala Pro Leu	Arg Met Tyr Asn Pro Thr
500		510
Thr Thr Leu Asn	Arg Glu Gln Glu Lys	Glu Pro Tyr Lys Asn Pro
515		525
Asn Leu Pro Leu	Ala Ala Ile Ile Gly	Gly Ala Val Ala Leu Val
530		540
Thr Ile Ala Leu	Leu Ala Leu Val Cys	Trp Tyr Val His Arg Asn
545		555
Gly Ser Leu Phe	Ser Arg Asn Cys Ala	Tyr Ser Lys Gly Arg Arg
560		570
Arg Lys Asp Asp	Tyr Ala Glu Ala Gly	Thr Lys Lys Asp Asn Ser
575		585
Ile Leu Glu Ile	Arg Glu Thr Ser Phe	Gln Met Leu Pro Ile Ser
590		600
Asn Glu Pro Ile	Ser Lys Glu Glu Phe	Val Ile His Thr Ile Phe
605		615
Pro Pro Asn Gly	Met Asn Leu Tyr Lys	Asn Asn His Ser Glu Ser
620		630

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Ser Ser Asn Arg Ser Tyr Arg Asp Ser Gly Ile Pro Asp Ser Asp
 635 640 645

His Ser His Ser

<210> SEQ ID NO 133

<211> LENGTH: 1882

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 133

ccgtcatccc cctgcagcca cccttcccag agtcctttgc ccaggccacc	50
ccaggcttct tggcagccct gccggggcac ttgtcttcat gtctgccagg	100
gggaggtggg aaggaggtgg gaggagggcg tgcagaggca gtctgggctt	150
ggccagagct cagggtgctg agcgtgtgac cagcagttag cagaggccgg	200
ccatggccag cctggggctg ctgctcctgc tcttactgac agcactgcca	250
ccgctgtggt cctcctcact gcctgggctg gacactgctg aaagtaaagc	300
caccattgca gacctgatcc tgtctgcgct ggagagagcc accgtcttcc	350
tagaacagag gctgcctgaa atcaacctgg atggcatggt gggggctccga	400
gtgctggaag agcagctaaa aagtgtccgg gagaagtggg cccaggagcc	450
cctgctgcag ccgctgagcc tgcgcgtggg gatgctgggg gagaagctgg	500
aggtgcccac ccagagatcc ctccactacc tcaagttagg tgatcccaag	550
tacctaagag agttccagct gacctccag cccgggtttt ggaagctccc	600
acatgcctgg atccacactg atgcctcctt ggtgtacccc acgttcgggc	650
cccaggactc attctcagag gagagaagtg acgtgtgcct ggtgcagctg	700
ctgggaaccg ggacggacag cagcgagccc tgcggcctct cagacctctg	750
caggagcctc atgaccaagc ccggtgctc aggtactgct ctgtcccacc	800
aactgctctt cttcctctgg gccagaatga ggggatgcac acagggacca	850
ctccaacaga gccaggacta tatcaacctc ttctgcgcca acatgatgga	900
cttgaaccgc agagctgagg ccatcgata cgcctaccct acccgggaca	950
tcttcatgga aaacatcatg ttctgtggaa tgggcggctt ctccgacttc	1000
tacaagctcc ggtggctgga ggccattctc agctggcaga aacagcagga	1050
aggatgcttc ggggagcctg atgctgaaga tgaagaatta tctaaagcta	1100
ttcaatatca gcagcatttt tcgaggagag tgaagaggcg agaaaaacaa	1150
tttcagatt ctgcctctgt tgctcaggct ggagtacagt ggcgcaatct	1200
cggctcactg caacctttgc ctccctgggt caagcaattc tcttgctca	1250
tcctcccag tagctgggac tacaggagcg tgccaccata cctggctaatt	1300
ttttatattt ttttagtaga gacagggttt catcatgttg ctcatgctgg	1350
tctogaactc ctgatctcaa gagatccgcc cacctcaggc tcccaaagtg	1400
tgggattata ggtgtgagcc accgtgtctg gctgaaaagc actttcaaag	1450
agactgtggt gaataaaggg ccaaggttct tgccaccag cactcatggg	1500
ggctctctcc cctagatggc tgctcctccc acaacacagc cacagcagtg	1550
gcagccctgg gtggcttcct atacatcctg gcagaatacc cccagcaaa	1600
cagagagcca caccatcca caccgccacc accaagcagc cgctgagacg	1650

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gacgggttcca tgccagctgc ctggaggagg aacagacccc tttagtcttc	1700
atcccttaga tcctggaggg cacggatcac atcctgggaa gaaggcatct	1750
ggaggataag caaagccacc ccgacaccca atcttgaag ccctgagtag	1800
gcagggccag ggtaggtggg ggccgggagg gacccaggtg tgaacggatg	1850
aataaagttc aactgcaact gaaaaaaaa aa	1882

<210> SEQ ID NO 134

<211> LENGTH: 440

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 134

Met	Ser	Ala	Arg	Gly	Arg	Trp	Glu	Gly	Gly	Gly	Arg	Arg	Ala	Cys	
1				5					10					15	
Arg	Gly	Ser	Leu	Gly	Leu	Ala	Arg	Ala	Gln	Gly	Ala	Glu	Arg	Val	
			20						25					30	
Thr	Ser	Ser	Glu	Gln	Arg	Pro	Ala	Met	Ala	Ser	Leu	Gly	Leu	Leu	
			35						40					45	
Leu	Leu	Leu	Leu	Leu	Thr	Ala	Leu	Pro	Pro	Leu	Trp	Ser	Ser	Ser	
			50						55					60	
Leu	Pro	Gly	Leu	Asp	Thr	Ala	Glu	Ser	Lys	Ala	Thr	Ile	Ala	Asp	
			65						70					75	
Leu	Ile	Leu	Ser	Ala	Leu	Glu	Arg	Ala	Thr	Val	Phe	Leu	Glu	Gln	
			80						85					90	
Arg	Leu	Pro	Glu	Ile	Asn	Leu	Asp	Gly	Met	Val	Gly	Val	Arg	Val	
			95						100					105	
Leu	Glu	Glu	Gln	Leu	Lys	Ser	Val	Arg	Glu	Lys	Trp	Ala	Gln	Glu	
			110						115					120	
Pro	Leu	Leu	Gln	Pro	Leu	Ser	Leu	Arg	Val	Gly	Met	Leu	Gly	Glu	
			125						130					135	
Lys	Leu	Glu	Ala	Ala	Ile	Gln	Arg	Ser	Leu	His	Tyr	Leu	Lys	Leu	
			140						145					150	
Ser	Asp	Pro	Lys	Tyr	Leu	Arg	Glu	Phe	Gln	Leu	Thr	Leu	Gln	Pro	
			155						160					165	
Gly	Phe	Trp	Lys	Leu	Pro	His	Ala	Trp	Ile	His	Thr	Asp	Ala	Ser	
			170						175					180	
Leu	Val	Tyr	Pro	Thr	Phe	Gly	Pro	Gln	Asp	Ser	Phe	Ser	Glu	Glu	
			185						190					195	
Arg	Ser	Asp	Val	Cys	Leu	Val	Gln	Leu	Leu	Gly	Thr	Gly	Thr	Asp	
			200						205					210	
Ser	Ser	Glu	Pro	Cys	Gly	Leu	Ser	Asp	Leu	Cys	Arg	Ser	Leu	Met	
			215						220					225	
Thr	Lys	Pro	Gly	Cys	Ser	Gly	Tyr	Cys	Leu	Ser	His	Gln	Leu	Leu	
			230						235					240	
Phe	Phe	Leu	Trp	Ala	Arg	Met	Arg	Gly	Cys	Thr	Gln	Gly	Pro	Leu	
			245						250					255	
Gln	Gln	Ser	Gln	Asp	Tyr	Ile	Asn	Leu	Phe	Cys	Ala	Asn	Met	Met	
			260						265					270	
Asp	Leu	Asn	Arg	Arg	Ala	Glu	Ala	Ile	Gly	Tyr	Ala	Tyr	Pro	Thr	
			275						280					285	
Arg	Asp	Ile	Phe	Met	Glu	Asn	Ile	Met	Phe	Cys	Gly	Met	Gly	Gly	
			290						295					300	
Phe	Ser	Asp	Phe	Tyr	Lys	Leu	Arg	Trp	Leu	Glu	Ala	Ile	Leu	Ser	

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305	310	315
Trp Gln Lys Gln Gln Glu Gly Cys Phe	Gly Glu Pro Asp Ala Glu	
320	325	330
Asp Glu Glu Leu Ser Lys Ala Ile Gln	Tyr Gln Gln His Phe Ser	
335	340	345
Arg Arg Val Lys Arg Arg Glu Lys Gln	Phe Pro Asp Ser Arg Ser	
350	355	360
Val Ala Gln Ala Gly Val Gln Trp Arg	Asn Leu Gly Ser Leu Gln	
365	370	375
Pro Leu Pro Pro Gly Phe Lys Gln Phe	Ser Cys Leu Ile Leu Pro	
380	385	390
Ser Ser Trp Asp Tyr Arg Ser Val Pro	Pro Tyr Leu Ala Asn Phe	
395	400	405
Tyr Ile Phe Leu Val Glu Thr Gly Phe	His His Val Ala His Ala	
410	415	420
Gly Leu Glu Leu Leu Ile Ser Arg Asp	Pro Pro Thr Ser Gly Ser	
425	430	435
Gln Ser Val Gly Leu		
440		

<210> SEQ ID NO 135

<211> LENGTH: 884

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 135

```

ggctctgagtg cagagctgct gtcattggcgg ccgctctgtg gggcttcttt      50
cccgtctctgc tgctgctgct gctatcgggg gatgtccaga gtcggagggt      100
gccccggggct gctgctgagg gatcgggagg gaggggggtc ggcataggag      150
atcgcttcaa gattgagggg cgtgcagttg ttccaggggt gaagcctcag      200
gactggatct cggcgggccc agtgctggta gacggagaag agcacgtcgg      250
tttccttaag acagatggga gttttgtggt tcatgatata ccttctggat      300
cttatgtagt ggaagtgtga tctccagctt acagatttga tccggttcga      350
gtggatatca cttcgaaagg aaaaatgaga gcaagatatg tgaattacat      400
caaaacatca gaggttgtca gactgcccta tcctctccaa atgaaatctt      450
cagggtccacc ttcttacttt attaaaaggg aatcgtgggg ctggacagac      500
tttctaataga acccaatggt tatgatgatg gttcttcctt tattgatatt      550
tgtgcttctg cctaaagtgg tcaacacaag tgatcctgac atgagacggg      600
aaatggagca gtcaatgaat atgctgaatt ccaaccatga gttgcctgat      650
gtttctgagt tcatgacaag actcttctct tcaaaatcat ctggcaaatc      700
tagcagcggc agcagtaaaa caggcaaaaag tggggctggc aaaaggaggt      750
agtcaggccg tccagagctg gcatttgac aaacacggca aactgggtg      800
gcatccaagt cttggaaaac cgtgtgaagc aactactata aacttgagtc      850
atcccgacgt tgatctctta caactgtgta tggt      884

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<210> SEQ ID NO 136

<211> LENGTH: 242

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 136

Met Ala Ala Ala Leu Trp Gly Phe Phe Pro Val Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Ser Gly Asp Val Gln Ser Ser Glu Val Pro Gly Ala Ala
 20 25 30
 Ala Glu Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Asp Arg Phe
 35 40 45
 Lys Ile Glu Gly Arg Ala Val Val Pro Gly Val Lys Pro Gln Asp
 50 55 60
 Trp Ile Ser Ala Ala Arg Val Leu Val Asp Gly Glu Glu His Val
 65 70 75
 Gly Phe Leu Lys Thr Asp Gly Ser Phe Val Val His Asp Ile Pro
 80 85 90
 Ser Gly Ser Tyr Val Val Glu Val Val Ser Pro Ala Tyr Arg Phe
 95 100 105
 Asp Pro Val Arg Val Asp Ile Thr Ser Lys Gly Lys Met Arg Ala
 110 115 120
 Arg Tyr Val Asn Tyr Ile Lys Thr Ser Glu Val Val Arg Leu Pro
 125 130 135
 Tyr Pro Leu Gln Met Lys Ser Ser Gly Pro Pro Ser Tyr Phe Ile
 140 145 150
 Lys Arg Glu Ser Trp Gly Trp Thr Asp Phe Leu Met Asn Pro Met
 155 160 165
 Val Met Met Met Val Leu Pro Leu Leu Ile Phe Val Leu Leu Pro
 170 175 180
 Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg Glu Met Glu
 185 190 195
 Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro Asp Val
 200 205 210
 Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly Lys
 215 220 225
 Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys
 230 235 240
 Arg Arg

<210> SEQ ID NO 137

<211> LENGTH: 1571

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 137

gatggcgcag ccacagcttc tgtgagattc gatttctccc cagttccoct 50
 gtgggtctga ggggaccaga agggtagact acgttggtt tctggaagg 100
 gaggtatat gcgtcaattc cccaaaacaa gttttgacat ttccccgaa 150
 atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200
 ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250
 cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300
 ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350
 tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400
 ctgcgtttta tctctatgg actccttcca ctggactgaa gacactcaat 450
 ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

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ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca	550
gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaatcga	600
tgctgcctcc tgcgccattt gctaagactc tatctggaca gggatattta	650
aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg	700
ccaattccctt tcttaccatc aagaaggacc tccggctctc tcatgcccac	750
atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct	800
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg	850
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa	900
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat	950
acctgcagag gaggcatgac cccaaaccac catctcttta ctgtactagt	1000
cttgctgctg tcacagtgtt tcttatttat gcattacttg cttccttgca	1050
tgattgtctt tatgcatccc caatcttaat tgagaccata cttgtataag	1100
atttttgtaa tatctttctg ctattggata tatttattag ttaatatatt	1150
tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa	1200
ctttaaaaaa attcacagat tatatttata acctgactag agcagggtgat	1250
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg	1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct	1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt	1400
tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga	1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg	1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata	1550
ccaaaaaaaa aaaaaaaaaa a	1571

<210> SEQ ID NO 138

<211> LENGTH: 261

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 138

Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met	
1 5 10 15	
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu	
20 25 30	
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys	
35 40 45	
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu	
50 55 60	
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu	
65 70 75	
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser	
80 85 90	
Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr	
95 100 105	
Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile	
110 115 120	
Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg	
125 130 135	

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Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
			140						145					150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
			155						160					165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
			170						175					180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
			185						190					195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
			200						205					210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
			215						220					225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
			230						235					240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
			245						250					255
Trp	Met	Glu	Glu	Thr	Glu									
					260									

<210> SEQ ID NO 139

<211> LENGTH: 2395

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 139

cctggagccg gaagcgcggc tgcagcaggg cgaggctcca ggtggggtcg	50
gttccgcata cagcctagcg tgtccacgat gcggctgggc tccgggactt	100
tcgctacctg ttgcgtagcg atcgaggtgc tagggatcgc ggtcttcttt	150
cggggattct tcccggctcc cgttcgttcc tctgccagag cggaacacgg	200
agcggagccc ccagcgccc aaccctcggc tggagccagt tctaactgga	250
ccacgctgcc accacctctc ttcagtaaag ttgttattgt tctgatagat	300
gccttgagag atgattttgt gtttgggtca aaggggtgtga aatttatgcc	350
ctacacaact taccttgtgg aaaaaggagc atctcacagt tttgtggctg	400
aagcaaaagg acctacagtt actatgcctc gaatcaaggc attgatgacg	450
gggagccttc ctggctttgt cgacgtcatc aggaacctca attctcctgc	500
actgctggaa gacagtgtga taagacaagc aaaagcagct ggaaaaagaa	550
tagtctttta tggagatgaa acctgggtta aattattccc aaagcatttt	600
gtggaatatg atggaacaac ctcatTTTTt gtgtcagatt acacagaggt	650
ggataataat gtcacgaggc atttggataa agtattaaaa agaggagatt	700
gggacatatt aatcctccac tacctggggc tggaccacat tggccacatt	750
tcagggccca acagcccct gattgggcag aagctgagcg agatggacag	800
cgtgctgatg aagatccaca cctcactgca gtcgaaggag agagagacgc	850
ctttacccaa tttgctggtt ctttgtgtg accatggcat gtctgaaaca	900
ggaagtacag gggcctcctc caccgaggag gtgaatacac ctctgatttt	950
aatcagttct gcgtttgaaa ggaaacccgg tgatatccga catccaaagc	1000
acgtccaata gacggatgtg gctgcgacac tggcgatagc acttggctta	1050
ccgattccaa aagacagtgt agggagcctc ctattcccag ttgtggaagg	1100

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aagaccaatg agagagcagt tgagatTTTT acatttgaat acagtgcagc      1150
ttagtaaact gttgcaagag aatgtgccgt catatgaaaa agatcctggg      1200
tttgagcagt ttaaaatgtc agaaagattg catgggaact ggatcagact      1250
gtacttggag gaaaagcatt cagaagtcct attcaacctg ggctccaagg      1300
ttctcaggca gtacctggat gctctgaaga cgctgagctt gtccctgagt      1350
gcacaagtgg cccagttctc accctgctcc tgctcagcgt cccacaggca      1400
ctgcacagaa aggctgagct ggaagtccca ctgtcatctc ctgggttttc      1450
tctgctcttt tatttggtga tcctggttct ttccggccgtt cagctcattg      1500
tgtgcacctc agctgaaagt tcgtgctact tctgtggcct ctcgtggctg      1550
gcggcaggct gcctttcgtt taccagactc tggttgaaca cctgggtgtg      1600
gccaaagtgt gccagtgccc tggacagggg gcctcagggg aggacgtgga      1650
gcagccttat cccaggcctc tgggtgtccc gacacaggtg ttcacatctg      1700
tgctgtcagg tcagatgcct cagttcttgg aaagctaggt tcctgcgact      1750
gttaccaagg tgattgtaaa gagctggcgg tcacagagga acaagccccc      1800
cagctgaggg ggtgtgtgaa tcggacagcc tcccagcaga ggtgtgggag      1850
ctgcagctga gggaagaaga gacaatcggc ctggacactc aggaggggtca      1900
aaaggagact tggtcgcacc actcatcctg ccccccag aatgcatect      1950
gcctcatcag gtccagattt ctttccaagg cggacgtttt ctgttgaat      2000
tcttagtcct tggcctcgga caccttcatt cgtagctgg ggagtgggtg      2050
tgaggcagtg aagaagaggg gtaggtgtac actcagatcc acagagccca      2100
ggatcaaggg acccactgca gtggcagcag gactgttggg cccccacccc      2150
aaccctgcac agccctcatc ccctcttggc ttgagccgtc agaggccctg      2200
tgctgagtgt ctgaccgaga cactcacagc tttgtcatca gggcacaggc      2250
ttcctcggag ccaggatgat ctgtgccagc cttgcacctc gggcccatct      2300
gggctcatgc tctctctcct gctattgaat tagtacctag ctgcacacag      2350
tatgtagtta ccaaaagaat aaacggcaat aattgagaaa aaaaa      2395

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<210> SEQ ID NO 140

<211> LENGTH: 310

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 140

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Met Arg Leu Gly Ser Gly Thr Phe Ala Thr Cys Cys Val Ala Ile
 1             5             10             15
Glu Val Leu Gly Ile Ala Val Phe Leu Arg Gly Phe Phe Pro Ala
 20            25            30
Pro Val Arg Ser Ser Ala Arg Ala Glu His Gly Ala Glu Pro Pro
 35            40            45
Ala Pro Glu Pro Ser Ala Gly Ala Ser Ser Asn Trp Thr Thr Leu
 50            55            60
Pro Pro Pro Leu Phe Ser Lys Val Val Ile Val Leu Ile Asp Ala
 65            70            75
Leu Arg Asp Asp Phe Val Phe Gly Ser Lys Gly Val Lys Phe Met
 80            85            90

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Pro	Tyr	Thr	Thr	Tyr	Leu	Val	Glu	Lys	Gly	Ala	Ser	His	Ser	Phe
				95					100					105
Val	Ala	Glu	Ala	Lys	Pro	Pro	Thr	Val	Thr	Met	Pro	Arg	Ile	Lys
				110					115					120
Ala	Leu	Met	Thr	Gly	Ser	Leu	Pro	Gly	Phe	Val	Asp	Val	Ile	Arg
				125					130					135
Asn	Leu	Asn	Ser	Pro	Ala	Leu	Leu	Glu	Asp	Ser	Val	Ile	Arg	Gln
				140					145					150
Ala	Lys	Ala	Ala	Gly	Lys	Arg	Ile	Val	Phe	Tyr	Gly	Asp	Glu	Thr
				155					160					165
Trp	Val	Lys	Leu	Phe	Pro	Lys	His	Phe	Val	Glu	Tyr	Asp	Gly	Thr
				170					175					180
Thr	Ser	Phe	Phe	Val	Ser	Asp	Tyr	Thr	Glu	Val	Asp	Asn	Asn	Val
				185					190					195
Thr	Arg	His	Leu	Asp	Lys	Val	Leu	Lys	Arg	Gly	Asp	Trp	Asp	Ile
				200					205					210
Leu	Ile	Leu	His	Tyr	Leu	Gly	Leu	Asp	His	Ile	Gly	His	Ile	Ser
				215					220					225
Gly	Pro	Asn	Ser	Pro	Leu	Ile	Gly	Gln	Lys	Leu	Ser	Glu	Met	Asp
				230					235					240
Ser	Val	Leu	Met	Lys	Ile	His	Thr	Ser	Leu	Gln	Ser	Lys	Glu	Arg
				245					250					255
Glu	Thr	Pro	Leu	Pro	Asn	Leu	Leu	Val	Leu	Cys	Gly	Asp	His	Gly
				260					265					270
Met	Ser	Glu	Thr	Gly	Ser	His	Gly	Ala	Ser	Ser	Thr	Glu	Glu	Val
				275					280					285
Asn	Thr	Pro	Leu	Ile	Leu	Ile	Ser	Ser	Ala	Phe	Glu	Arg	Lys	Pro
				290					295					300
Gly	Asp	Ile	Arg	His	Pro	Lys	His	Val	Gln					
				305					310					

<210> SEQ ID NO 141

<211> LENGTH: 754

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 141

ggcacgaggc aagccttcca ggttatcgtg acgcaccttg aaagtctgag	50
agctactgcc ctacagaaag ttactagtgc cctaaagctg gcgctggcac	100
tgatgttact gctgctgttg gagtacaact tccctataga aaacaactgc	150
cagcacctta agaccactca caccttcaga gtgaagaact taaacccgaa	200
gaaattcagc attcatgacc aggatcacia agtactggtc ctggactctg	250
ggaatctcat agcagttcca gataaaaact acatacgccc agagatcttc	300
tttgcattag cctcatcctt gagctcagcc tctgcggaga aaggaagtcc	350
gattctcctg ggggtctcta aaggggagtt ttgtctctac tgtgacaagg	400
ataaaggaca aagtcattcca tcccttcagc tgaagaagga gaaactgatg	450
aagctggctg cccaaaagga atcagcacgc cggcccttca tcttttatag	500
ggctcaggtg ggctcctgga acatgctgga gtcggcggct caccgccgat	550
ggttcactctg cacctcctgc aattgtaatg agcctgttgg ggtgacagat	600
aaatttgaga acaggaaca cattgaattt tcatttcaac cagtttgcaa	650

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agctgaaatg agccccagtg aggtcagcga ttaggaaact gccccattga      700
acgccttcct cgctaatttg aactaattgt ataaaaacac caaacctgct      750
cact                                                            754

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<210> SEQ ID NO 142
<211> LENGTH: 193
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 142

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Met Leu Leu Leu Leu Leu Glu Tyr Asn Phe Pro Ile Glu Asn Asn
  1             5             10             15
Cys Gln His Leu Lys Thr Thr His Thr Phe Arg Val Lys Asn Leu
             20             25             30
Asn Pro Lys Lys Phe Ser Ile His Asp Gln Asp His Lys Val Leu
             35             40             45
Val Leu Asp Ser Gly Asn Leu Ile Ala Val Pro Asp Lys Asn Tyr
             50             55             60
Ile Arg Pro Glu Ile Phe Phe Ala Leu Ala Ser Ser Leu Ser Ser
             65             70             75
Ala Ser Ala Glu Lys Gly Ser Pro Ile Leu Leu Gly Val Ser Lys
             80             85             90
Gly Glu Phe Cys Leu Tyr Cys Asp Lys Asp Lys Gly Gln Ser His
             95            100            105
Pro Ser Leu Gln Leu Lys Lys Glu Lys Leu Met Lys Leu Ala Ala
            110            115            120
Gln Lys Glu Ser Ala Arg Arg Pro Phe Ile Phe Tyr Arg Ala Gln
            125            130            135
Val Gly Ser Trp Asn Met Leu Glu Ser Ala Ala His Pro Gly Trp
            140            145            150
Phe Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro Val Gly Val Thr
            155            160            165
Asp Lys Phe Glu Asn Arg Lys His Ile Glu Phe Ser Phe Gln Pro
            170            175            180
Val Cys Lys Ala Glu Met Ser Pro Ser Glu Val Ser Asp
            185            190

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<210> SEQ ID NO 143
<211> LENGTH: 961
<212> TYPE: DNA
<213> ORGANISM: Homo Sapien

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<400> SEQUENCE: 143

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ctagagagta tagggcagaa ggatggcaga tgagtgactc cacatccaga      50
gtgcctccc tttaatccag gatcctgtcc ttcctgtcct gtaggagtgc      100
ctgttgccag tgtgggggtga gacaagtttg tcccacaggg ctgtctgagc      150
agataagatt aagggtggg tctgtgtcga attaactcct gtgggcacgg      200
gggctgggaa gagcaaagtc agcgtgcct acagtcagca ccatgctggg      250
cctgccgtgg aaggagggtc tgtcctgggc gctgctgctg cttctcttag      300
gtcccagat cctgctgac tatgcctggc atttcacga gcaaaggagc      350
tgtgatgaac acaatgtcat ggctcgttac ctccctgcc cagtggagtt      400
tgctgtccac acattcaacc aacagagcaa ggactactat gcctacagac      450

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tggggcacat cttgaattcc tggaaggagc aggtggagtc caagactgta	500
ttctcaatgg agctactgct ggggagaact aggtgtggga aatttgaaga	550
cgacattgac aactgccatt tccaagaaag cacagagctg aacaatactt	600
tcacctgctt cttcaccatc agcaccaggc cctggatgac tcagttcagc	650
ctcctgaaca agacctgctt ggagggatc cactgagtga aaccactca	700
caggcttgtc catgtgctgc tcccacatc cgtggacatc agcactactc	750
tcctgaggac tcttcagtgg ctgagcagct ttggacttgt ttgttatcct	800
attttgcatg tgtttgagat ctcagatcag tgttttagaa aatccacaca	850
tcttgagcct aatcatgtag tgtagatcat taaacatcag cattttaaga	900
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	950
aaaaaaaaa a	961

<210> SEQ ID NO 144

<211> LENGTH: 147

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 144

Met Leu Gly Leu Pro Trp Lys Gly Gly Leu Ser Trp Ala Leu Leu	1	5	10	15
Leu Leu Leu Leu Gly Ser Gln Ile Leu Leu Ile Tyr Ala Trp His	20	25	30	
Phe His Glu Gln Arg Asp Cys Asp Glu His Asn Val Met Ala Arg	35	40	45	
Tyr Leu Pro Ala Thr Val Glu Phe Ala Val His Thr Phe Asn Gln	50	55	60	
Gln Ser Lys Asp Tyr Tyr Ala Tyr Arg Leu Gly His Ile Leu Asn	65	70	75	
Ser Trp Lys Glu Gln Val Glu Ser Lys Thr Val Phe Ser Met Glu	80	85	90	
Leu Leu Leu Gly Arg Thr Arg Cys Gly Lys Phe Glu Asp Asp Ile	95	100	105	
Asp Asn Cys His Phe Gln Glu Ser Thr Glu Leu Asn Asn Thr Phe	110	115	120	
Thr Cys Phe Phe Thr Ile Ser Thr Arg Pro Trp Met Thr Gln Phe	125	130	135	
Ser Leu Leu Asn Lys Thr Cys Leu Glu Gly Phe His	140	145		

<210> SEQ ID NO 145

<211> LENGTH: 1157

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 145

ctgtgcagct cgaggctcca gaggcacact ccagagagag ccaaggttct	50
gacgcgatga ggaagcacct gagctggtgg tggctggcca ctgtctgcat	100
gctgctcttc agccacctct ctgcggtcca gacgaggggc atcaagcaca	150
gaatcaagtg gaaccggaag gccctgcccc gactgcccc gatcactgag	200
gcccaggtgg ctgagaaccg cccgggagcc ttcataaagc aaggccgcaa	250
gctcgacatt gacttcggag ccgagggcaa caggtactac gaggccaaact	300

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actggcagtt ccccgatggc atccactaca acggctgctc tgaggctaatt      350
gtgaccaagg aggcatttgt caccggctgc atcaatgccca cccaggcggc      400
gaaccagggg gagttccaga agccagacaa caagctccac cagcaggtgc      450
tctggcggct ggtccaggag ctctgctccc tcaagcattg cgagtttttg      500
ttggagaggg gcgcaggact tcgggtcacc atgcaccagc cagtgtctct      550
ctgccttctg gctttgatct ggctcatggt gaaataagct tgccaggagg      600
ctggcagtac agagcgagc agcgagcaaa tcctggcaag tgaccagct      650
cttctccccc aaaccacgc gtgttctgaa ggtgcccagg agcggcgatg      700
cactcgcaact gcaaatgccg ctcccacgta tgcgccctgg tatgtgcctg      750
cgttctgata gatgggggac tgtggcttct ccgtcactcc attctcagcc      800
cctagcagag cgtctggcac actagattag tagtaaatgc ttgatgagaa      850
gaacacatca ggcactgcgc cacctgcttc acagtacttc ccaacaactc      900
ttagaggtag gtgtattccc gttttacaga taaggaaact gagggccaga      950
gagctgaagt actgcaccca gcatcaccag ctagaaagtg gcagagccag     1000
gattcaaccc tggcttgtct aaccccaggt tttctgctct gtccaattcc     1050
agagctgtct ggtgatcact ttatgtctca cagggacca catccaaaca     1100
tgtatctcta atgaaattgt gaaagctcca tgtttagaaa taaatgaaaa     1150
cacctga                                           1157

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<210> SEQ ID NO 146

<211> LENGTH: 176

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 146

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Met Arg Lys His Leu Ser Trp Trp Trp Leu Ala Thr Val Cys Met
  1             5             10             15
Leu Leu Phe Ser His Leu Ser Ala Val Gln Thr Arg Gly Ile Lys
             20             25             30
His Arg Ile Lys Trp Asn Arg Lys Ala Leu Pro Ser Thr Ala Gln
             35             40             45
Ile Thr Glu Ala Gln Val Ala Glu Asn Arg Pro Gly Ala Phe Ile
             50             55             60
Lys Gln Gly Arg Lys Leu Asp Ile Asp Phe Gly Ala Glu Gly Asn
             65             70             75
Arg Tyr Tyr Glu Ala Asn Tyr Trp Gln Phe Pro Asp Gly Ile His
             80             85             90
Tyr Asn Gly Cys Ser Glu Ala Asn Val Thr Lys Glu Ala Phe Val
             95             100            105
Thr Gly Cys Ile Asn Ala Thr Gln Ala Ala Asn Gln Gly Glu Phe
            110            115            120
Gln Lys Pro Asp Asn Lys Leu His Gln Gln Val Leu Trp Arg Leu
            125            130            135
Val Gln Glu Leu Cys Ser Leu Lys His Cys Glu Phe Trp Leu Glu
            140            145            150
Arg Gly Ala Gly Leu Arg Val Thr Met His Gln Pro Val Leu Leu
            155            160            165
Cys Leu Leu Ala Leu Ile Trp Leu Met Val Lys

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170

175

<210> SEQ ID NO 147
 <211> LENGTH: 333
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 147

gccttggcct cccaaagggc tgggattata ggcgtgacca ccatgtctgg	50
tccagagtct catcttcctga tgatttatag actcaaagaa aactcatgtt	100
cagaagctct ctctctctct ggcctcctct ctgtcttctt tccctctttc	150
ttcttatttt aattagtagc atctactcag agtcatgcaa gctggaaatc	200
tttcattttg ctgtgcagtg gggtaggtca ctgagtctta gtttttattt	250
tttgaaattt caactttcag attcaggggg tacatgtgaa ggtttgtttt	300
atgagtatat tgcatgatgc tgaggtttgg ggt	333

<210> SEQ ID NO 148
 <211> LENGTH: 73
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 148

Met Phe Arg Ser Ser Leu Leu Phe Trp Pro Pro Leu Cys Leu Leu	
1 5 10 15	
Ser Leu Phe Leu Leu Ile Leu Ile Ser Ser Ile Tyr Ser Glu Ser	
20 25 30	
Cys Lys Leu Glu Ile Phe His Phe Ala Cys Gln Trp Gly Arg Ser	
35 40 45	
Leu Ser Leu Ser Phe Tyr Phe Leu Lys Phe Gln Leu Ser Asp Ser	
50 55 60	
Gly Gly Thr Cys Glu Gly Leu Phe Tyr Glu Tyr Ile Ala	
65 70	

<210> SEQ ID NO 149
 <211> LENGTH: 1893
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 149

gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgctcccc	50
tctacctgga gacttgactc ccgcgcgccc caaccctgct tatcccttga	100
ccgtcagagtg tcagagatcc tgcagccgcc cagtcccggc ccctctcccg	150
ccccacaccc accctcctgg ctcttctctgt ttttactcct ccttttcatt	200
cataacaaaa gctacagctc caggagccca gcgccgggct gtgaccaaac	250
ccgagcgtgg aagaatgggg ttcctcgga cgggcacttg gattctggtg	300
ttagtgtcc cgattcaagc tttccocaaa cctggaggaa gccaaagaaa	350
atctctacat aatagagaat taagtgcaga aagacctttg aatgaacaga	400
ttgctgaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac	450
aagccaggtc agagcaacta ttcttttgtt gataacttga acctgctaaa	500
ggcaataaca gaaaaggaaa aaattgagaa agaaagacaa tctataagaa	550
gctccccact tgataataag ttgaatgtgg aagatgttga ttcaaccaag	600

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aatcgaaaaa	tgatcgatga	ttatgactct	actaagagtg	gattggatca	650
taaaattcaa	gatgatccag	atggtcttca	tcaactagac	gggactcctt	700
taaccgctga	agacattgtc	cataaaatcg	ctgccaggat	ttatgaagaa	750
aatgacagag	ccgtgtttga	caagattggt	tctaaactac	ttaatctcgg	800
ccttatcaca	gaaagccaag	cacatacact	ggaagatgaa	gtagcagagg	850
ttttacaaaa	attaatctca	aaggaagcca	acaattatga	ggaggatccc	900
aataagccca	caagctggac	tgagaatcag	gctggaaaaa	taccagagaa	950
agtgactcca	atggcagcaa	ttcaagatgg	tcttgctaag	ggagaaaacg	1000
atgaaacagt	atctaacaca	ttaaccttga	caaattggctt	ggaaaggaga	1050
actaaaaact	acagtgaaga	caactttgag	gaactccaat	atttcccaaa	1100
tttctatgcg	ctactgaaaa	gtattgattc	agaaaaagaa	gcaaaagaga	1150
aagaaacact	gattactatc	atgaaaacac	tgattgactt	tgtgaagatg	1200
atggtgaaat	atggaacaat	atctccagaa	gaaggtgttt	cctaccttga	1250
aaacttggat	gaaatgattg	ctcttcagac	caaaaacaag	ctagaaaaaa	1300
atgctactga	caatataagc	aagcttttcc	cagcaccatc	agagaagagt	1350
catgaagaaa	cagacagtac	caaggaagaa	gcagctaaga	tggaaaagga	1400
atatggaagc	ttgaaggatt	ccacaaaaga	tgataactcc	aacctcaggag	1450
gaaagacaga	tgaaccctaa	ggaaaaacag	aagcctatct	ggaagccatc	1500
agaaaaaata	ttgaatggtt	gaagaaacat	gacaaaaagg	gaaataaaga	1550
agattatgac	ctttcaaaga	tgagagactt	catcaataaa	caagctgatg	1600
cttatgtgga	gaaaggcatc	cttgacaagg	aagaagccga	ggccatcaag	1650
cgcatttata	gcagcctgta	aaaatggcaa	aagatccagg	agtctttcaa	1700
ctgtttcaga	aaacataata	tagcttaaaa	cacttctaata	tctgtgatta	1750
aaatTTTTTg	acccaagggt	tattagaaag	tgctgaattt	acagtagtta	1800
accttttaca	agtgggttaa	acatagcttt	cttcccgtaa	aaactatctg	1850
aaagtaaagt	tgtatgtaag	ctgaaaaaaa	aaaaaaaaaa	aaa	1893

<210> SEQ ID NO 150

<211> LENGTH: 468

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 150

Met	Gly	Phe	Leu	Gly	Thr	Gly	Thr	Trp	Ile	Leu	Val	Leu	Val	Leu
1				5					10					15
Pro	Ile	Gln	Ala	Phe	Pro	Lys	Pro	Gly	Gly	Ser	Gln	Asp	Lys	Ser
				20					25					30
Leu	His	Asn	Arg	Glu	Leu	Ser	Ala	Glu	Arg	Pro	Leu	Asn	Glu	Gln
				35					40					45
Ile	Ala	Glu	Ala	Glu	Glu	Asp	Lys	Ile	Lys	Lys	Thr	Tyr	Pro	Pro
				50					55					60
Glu	Asn	Lys	Pro	Gly	Gln	Ser	Asn	Tyr	Ser	Phe	Val	Asp	Asn	Leu
				65					70					75
Asn	Leu	Leu	Lys	Ala	Ile	Thr	Glu	Lys	Glu	Lys	Ile	Glu	Lys	Glu
				80					85					90
Arg	Gln	Ser	Ile	Arg	Ser	Ser	Pro	Leu	Asp	Asn	Lys	Leu	Asn	Val

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95					100					105				
Glu	Asp	Val	Asp	Ser	Thr	Lys	Asn	Arg	Lys	Leu	Ile	Asp	Asp	Tyr
				110					115					120
Asp	Ser	Thr	Lys	Ser	Gly	Leu	Asp	His	Lys	Phe	Gln	Asp	Asp	Pro
				125					130					135
Asp	Gly	Leu	His	Gln	Leu	Asp	Gly	Thr	Pro	Leu	Thr	Ala	Glu	Asp
				140					145					150
Ile	Val	His	Lys	Ile	Ala	Ala	Arg	Ile	Tyr	Glu	Glu	Asn	Asp	Arg
				155					160					165
Ala	Val	Phe	Asp	Lys	Ile	Val	Ser	Lys	Leu	Leu	Asn	Leu	Gly	Leu
				170					175					180
Ile	Thr	Glu	Ser	Gln	Ala	His	Thr	Leu	Glu	Asp	Glu	Val	Ala	Glu
				185					190					195
Val	Leu	Gln	Lys	Leu	Ile	Ser	Lys	Glu	Ala	Asn	Asn	Tyr	Glu	Glu
				200					205					210
Asp	Pro	Asn	Lys	Pro	Thr	Ser	Trp	Thr	Glu	Asn	Gln	Ala	Gly	Lys
				215					220					225
Ile	Pro	Glu	Lys	Val	Thr	Pro	Met	Ala	Ala	Ile	Gln	Asp	Gly	Leu
				230					235					240
Ala	Lys	Gly	Glu	Asn	Asp	Glu	Thr	Val	Ser	Asn	Thr	Leu	Thr	Leu
				245					250					255
Thr	Asn	Gly	Leu	Glu	Arg	Arg	Thr	Lys	Thr	Tyr	Ser	Glu	Asp	Asn
				260					265					270
Phe	Glu	Glu	Leu	Gln	Tyr	Phe	Pro	Asn	Phe	Tyr	Ala	Leu	Leu	Lys
				275					280					285
Ser	Ile	Asp	Ser	Glu	Lys	Glu	Ala	Lys	Glu	Lys	Glu	Thr	Leu	Ile
				290					295					300
Thr	Ile	Met	Lys	Thr	Leu	Ile	Asp	Phe	Val	Lys	Met	Met	Val	Lys
				305					310					315
Tyr	Gly	Thr	Ile	Ser	Pro	Glu	Glu	Gly	Val	Ser	Tyr	Leu	Glu	Asn
				320					325					330
Leu	Asp	Glu	Met	Ile	Ala	Leu	Gln	Thr	Lys	Asn	Lys	Leu	Glu	Lys
				335					340					345
Asn	Ala	Thr	Asp	Asn	Ile	Ser	Lys	Leu	Phe	Pro	Ala	Pro	Ser	Glu
				350					355					360
Lys	Ser	His	Glu	Glu	Thr	Asp	Ser	Thr	Lys	Glu	Glu	Ala	Ala	Lys
				365					370					375
Met	Glu	Lys	Glu	Tyr	Gly	Ser	Leu	Lys	Asp	Ser	Thr	Lys	Asp	Asp
				380					385					390
Asn	Ser	Asn	Pro	Gly	Gly	Lys	Thr	Asp	Glu	Pro	Lys	Gly	Lys	Thr
				395					400					405
Glu	Ala	Tyr	Leu	Glu	Ala	Ile	Arg	Lys	Asn	Ile	Glu	Trp	Leu	Lys
				410					415					420
Lys	His	Asp	Lys	Lys	Gly	Asn	Lys	Glu	Asp	Tyr	Asp	Leu	Ser	Lys
				425					430					435
Met	Arg	Asp	Phe	Ile	Asn	Lys	Gln	Ala	Asp	Ala	Tyr	Val	Glu	Lys
				440					445					450
Gly	Ile	Leu	Asp	Lys	Glu	Glu	Ala	Glu	Ala	Ile	Lys	Arg	Ile	Tyr
				455					460					465

Ser Ser Leu

<210> SEQ ID NO 151

<211> LENGTH: 2598

-continued

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 151

cggctcgagg ctcccgccag gagaaaggaa cattctgagg ggagtctaca	50
ccctgtggag ctcaagatgg tcctgagtg ggcgctgtgc ttccgaatga	100
aggactcggc attgaaggtg ctttatctgc ataataacca gcttctagct	150
ggagggctgc atgcagggaa ggtcattaaa ggtgaagaga tcagcgtggt	200
ccccaatcgg tggctggatg ccagcctgtc ccccgctatc ctgggtgtcc	250
aggggtggaag ccagtgcctg tcatgtgggg tggggcagga gccgactcta	300
acactagagc cagtgaacat catggagctc tatcttggtg ccaaggaatc	350
caagagcttc accttctacc ggcgggacat ggggctcacc tccagcttcg	400
agtcggctgc ctacccgggc tgggtcctgt gcacgggtgcc tgaagccgat	450
cagcctgtca gactcaccga gcttcccag aatggtggct ggaatgcccc	500
catcacagac ttctacttcc agcagtgatg ctagggaac gtgcccccca	550
gaactccctg ggcagagcca gctcgggtga ggggtgagtg gagagaccc	600
atggcggaca atcactctct ctgctctcag gacccccacg tctgacttag	650
tgggcacctg accactttgt cttctggttc ccagtttga taaattctga	700
gatttgagc tcagtccacg gtccctcccc actggatggt gctactgctg	750
tggaaccttg taaaaacat gtggggtaaa ctgggaataa catgaaaaga	800
tttctgtggg ggtgggtgg gggagtgtg ggaatcattc ctgcttaatg	850
gtaactgaca agtgttacct tgagccccgc aggcccaacc atccccagtt	900
gagccttata gggtcagtag ctctccacat gaagtcctgt cactcaccac	950
tgtgcaggag agggaggtg tcatagatgc agggatctat ggccttggc	1000
ccagccccac ccccttcctt ttaatcctgc cactgtcata tgctaccttt	1050
cctatctctt ccctcatcat cttgttgtg gcattgaggag gtggtgatgt	1100
cagaagaaat ggctcgagct cagaagataa aagataagta gggtagctg	1150
atcctctttt aaaaacccaa gatacaatca aaatcccaga tgctggtctc	1200
tattcccatg aaaaagtgtc catgacatat tgagaagacc tacttacaaa	1250
gtggcatata ttgcaattta ttttaattaa aagataccta tttatatatt	1300
tctttataga aaaaagtctg gaagagtta cttcaattgt agcaatgtca	1350
gggtgtgtgc agtatagggt atttttcttt taattctggt aatttatctg	1400
tatttcctaa tttttctaca atgaagatga attccttgta taaaaataag	1450
aaaagaaatt aatcttgagg taagcagagc agacatcatc tctgattgtc	1500
ctcagcctcc acttccccag agtaaattca aattgaatcg agctctgctg	1550
ctctggttgg ttgtagtagt gatcaggaaa cagatctcag caaagccact	1600
gaggaggagg ctgtgctgag tttgtgtggc tggaatctct gggtaggaa	1650
cttaaagaac aaaaatcatc tggtaattct ttcctagaag gatcacagcc	1700
cctgggattc caaggcattg gatccagtct ctaagaaggc tgctgtactg	1750
gttgaattgt gtccccctca aattcacatc cttcttgtaa tctcagctg	1800
tgagtttatt tggagataag gtctctgcag atgtagttag ttaagacaag	1850

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gtcatgctgg atgaaggtag acctaaattc aatatgactg gtttccttgt	1900
atgaaaagga gaggacacag agacagagga gacgcgggga agactatgta	1950
aagatgaagg cagagatcgg agttttgcag ccacaagcta agaaacacca	2000
aggattgtgg caaccatcag aagcttggaa gaggcaaaga agaattcttc	2050
cctagaggct ttagagggat aacggctctg ctgaaacctt aatctcagac	2100
ttccagcctc ctgaacgaag aaagaataaa tttcggctgt ttttaagccac	2150
caaggataat tggttacagc agctctagga aactaatata gctgctaaaa	2200
tgatccctgt ctctcgtgt ttacattctg tgtgtgtccc ctcccacaat	2250
gtaccaaagt tgtctttgtg accaatagaa tatggcagaa gtgatggcat	2300
gccacttcca agattaggtt ataaaagaca ctgcagcttc tacttgagcc	2350
ctctctctct gccacccacc gcccacaatc tatcttggt cactcgtct	2400
gggggaagct agctgccatg ctatgagcag gcctataaag agacttacgt	2450
ggtaaaaaat gaagtctcct gccacagccc acattagtga acctagaagc	2500
agagactctg tgagataatc gatgtttgtt gttttaagtt gctcagtttt	2550
ggtctaactt gttatgcagc aatagataaa taatatgcag agaagag	2598

<210> SEQ ID NO 152

<211> LENGTH: 155

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 152

Met Val Leu Ser Gly	Ala Leu Cys Phe Arg	Met Lys Asp Ser Ala
1	5	10 15
Leu Lys Val Leu Tyr	Leu His Asn Asn Gln	Leu Leu Ala Gly Gly
20	25	30
Leu His Ala Gly Lys	Val Ile Lys Gly Glu	Glu Ile Ser Val Val
35	40	45
Pro Asn Arg Trp Leu	Asp Ala Ser Leu Ser	Pro Val Ile Leu Gly
50	55	60
Val Gln Gly Gly Ser	Gln Cys Leu Ser Cys	Gly Val Gly Gln Glu
65	70	75
Pro Thr Leu Thr Leu	Glu Pro Val Asn Ile	Met Glu Leu Tyr Leu
80	85	90
Gly Ala Lys Glu Ser	Lys Ser Phe Thr Phe	Tyr Arg Arg Asp Met
95	100	105
Gly Leu Thr Ser Ser	Phe Glu Ser Ala Ala	Tyr Pro Gly Trp Phe
110	115	120
Leu Cys Thr Val Pro	Glu Ala Asp Gln Pro	Val Arg Leu Thr Gln
125	130	135
Leu Pro Glu Asn Gly	Gly Trp Asn Ala Pro	Ile Thr Asp Phe Tyr
140	145	150
Phe Gln Gln Cys Asp		
155		

<210> SEQ ID NO 153

<211> LENGTH: 1152

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 153

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cttcagaaca ggttctcctt cccagtcac cagttgctcg agttagaatt	50
gtctgcaatg gccgccctgc agaaatctgt gagctctttc cttatgggga	100
ccctggccac cagctgcctc cttctcttgg ccctcttggt acagggagga	150
gcagctgcgc ccatacagtc ccaactgcagg cttgacaagt ccaacttcca	200
gcagccctat atcaccaacc gcaccttcat gctggctaag gaggctagct	250
tggttgataa caacacagac gttcgtctca ttggggagaa actgttccac	300
ggagtcagta tgagtgcgc ctgctatctg atgaagcagg tgctgaactt	350
caccctgaa gaagtgcgtg tccctcaatc tgatagggtc cagccttata	400
tgaggagggt ggtgcccttc ctggccaggc tcagcaacag gctaagcaca	450
tgctcatattg aaggatga cctgcatac cagaggaatg tgcaaaagct	500
gaaggacaca gtgaaaaagc ttggagagag tggagagatc aaagcaattg	550
gagaactgga ttgtctgtt atgtctctga gaaatgcctg catttgacca	600
gagcaaaagct gaaaaatgaa taactaacc cctttccctg ctgaaaataa	650
caattagatg ccccaaagcg atttttttta accaaaagga agatgggaag	700
ccaaactcca tcatgatggg tggattccaa atgaaccct gcgttagtta	750
caaaggaaac caatgccact ttgtttata agaccagaag gtgactttc	800
taagcataga tatttattga taacatttca ttgtaactgg tgttctatac	850
acagaaaaca atttattttt taaataattg tctttttcca taaaaagat	900
tactttccat tccttttagg gaaaaaacc ctaaatagct tcactgttcc	950
ataatcagta ctttatattt ataaatgtat ttattattat tataagactg	1000
cattttattt atatcatttt attaatatgg atttatttat agaacatca	1050
ttcgatattg ctacttgagt gtaaggctaa tattgatatt tatgacaata	1100
attatagagc tataacatgt ttatttgacc tcaataaaca cttggatatc	1150
cc	1152

<210> SEQ ID NO 154

<211> LENGTH: 179

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 154

Met	Ala	Ala	Leu	Gln	Lys	Ser	Val	Ser	Ser	Phe	Leu	Met	Gly	Thr
1				5						10				15
Leu	Ala	Thr	Ser	Cys	Leu	Leu	Leu	Leu	Ala	Leu	Leu	Val	Gln	Gly
				20					25					30
Gly	Ala	Ala	Ala	Pro	Ile	Ser	Ser	His	Cys	Arg	Leu	Asp	Lys	Ser
				35					40					45
Asn	Phe	Gln	Gln	Pro	Tyr	Ile	Thr	Asn	Arg	Thr	Phe	Met	Leu	Ala
				50					55					60
Lys	Glu	Ala	Ser	Leu	Ala	Asp	Asn	Asn	Thr	Asp	Val	Arg	Leu	Ile
				65					70					75
Gly	Glu	Lys	Leu	Phe	His	Gly	Val	Ser	Met	Ser	Glu	Arg	Cys	Tyr
				80					85					90
Leu	Met	Lys	Gln	Val	Leu	Asn	Phe	Thr	Leu	Glu	Glu	Val	Leu	Phe
				95					100					105
Pro	Gln	Ser	Asp	Arg	Phe	Gln	Pro	Tyr	Met	Gln	Glu	Val	Val	Pro
				110					115					120

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Phe Leu Ala Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu
 125 130 135

Gly Asp Asp Leu His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp
 140 145 150

Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly
 155 160 165

Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Ile
 170 175

<210> SEQ ID NO 155
 <211> LENGTH: 1320
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 155

ggcttgctga aaataaaatc aggactccta acctgctcca gtcagcctgc	50
ttccacgagg cctgtcagtc agtgcccgac ttgtgactga gtgtgcagtg	100
cccagcatgt accaggtcag tcagaggggc tgcctgaggg ctgtgctgag	150
agggagagga gcagagatgc tgctgagggg ggagggaggc caagctgcca	200
ggtttggggc tgggggccaa gtggagttag aaactgggat cccaggggga	250
gggtgcagat gaggagcgca cccagattag gtgaggacag ttctctcatt	300
agccttttcc tacaggtggt tgcattcttg gcaatggtca tgggaaccca	350
cacctacagc cactggccca gctgctgccc cagcaaaggg caggacacct	400
ctgaggagct gctgaggtgg agcactgtgc ctgtgcctcc cctagagcct	450
gctaggccca accgccaccc agagtccctg agggccagtg aagatggacc	500
cctcaacagc agggccatct cccctggag atatgagttg gacagagact	550
tgaaccggct ccccaggac ctgtaccacg cccgttgctt gtgcccgcac	600
tgcgtcagcc tacagacagg ctcccacatg gacccccggg gcaactcgga	650
gctgctctac cacaaccaga ctgtcttcta caggcggcca tgccatggcg	700
agaagggcac ccacaaggc tactgcctgg agcgaggct gtaccgtgtt	750
tccttagctt gtgtgtgtgt gcggccccgt gtgatgggct agccggacct	800
gctggaggct ggtccctttt tgggaaacct ggagccaggt gtacaaccac	850
ttgccatgaa gggccaggat gcccagatgc ttggccccctg tgaagtgtg	900
tctggagcag caggatcccc ggacaggatg gggggctttg gggaaaacct	950
gcacttctgc acattttgaa aagagcagct gctgcttagg gccgccgga	1000
gctgggtgcc tgtcatthtc tctcaggaaa ggttttcaa gttctgcca	1050
tttctggagg ccaccactcc tgtctcttcc tcttttccca tcccctgcta	1100
ccctggccca gcacaggcac tttctagata tttccccctt gctggagaag	1150
aaagagcccc tggttttatt tgtttgttta ctcactactc agtgagcatc	1200
tactttgggt gcattctagt gtagttacta gtcttttgac atggatgatt	1250
ctgaggagga agctgttatt gaatgtatag agatttatcc aaataaatat	1300
ctttatttaa aaatgaaaaa	1320

<210> SEQ ID NO 156
 <211> LENGTH: 177
 <212> TYPE: PRT

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<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 156

```

Met Arg Glu Arg Pro Arg Leu Gly Glu Asp Ser Ser Leu Ile Ser
 1           5           10           15
Leu Phe Leu Gln Val Val Ala Phe Leu Ala Met Val Met Gly Thr
 20           25           30
His Thr Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln
 35           40           45
Asp Thr Ser Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro
 50           55           60
Pro Leu Glu Pro Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg
 65           70           75
Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp
 80           85           90
Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro Gln Asp Leu
 95          100          105
Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu Gln Thr
110          115          120
Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr His
125          130          135
Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly
140          145          150
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser
155          160          165
Leu Ala Cys Val Cys Val Arg Pro Arg Val Met Gly
170          175

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<210> SEQ ID NO 157

<211> LENGTH: 1515

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 157

```

ccggcgatgt cgctcgtgct gctaagcctg gccgcgctgt gcaggagcgc          50
cgtaccccca gagccgaccg ttcaatgtgg ctctgaaact gggccatctc          100
cagagtggat gctacaacat gatctaattc ccggagactt gagggacctc          150
cgagtagaac ctgttacaac tagtgttgca acaggggact attcaatttt          200
gatgaatgta agctgggtac tccgggcaga tgccagcatc cgcttggtga          250
aggccaccaa gatattgtgt acgggcacaaa gcaacttcca gtcctacagc          300
tgtgtgaggt gcaattacac agaggccttc cagactcaga ccagaccctc          350
tggttgtaaa tggacatttt cctacatcgg cttccctgta gagctgaaca          400
cagtctatatt cattggggcc cataatattc ctaatgcaaa tatgaatgaa          450
gatggccctt ccatgtctgt gaatttcacc tcaccaggct gcctagacca          500
cataatgaaa tataaaaaaa agtgtgtcaa ggccggaagc ctgtgggatc          550
cgaacatcac tgcttgtaag aagaatgagg agacagtaga agtgaacttc          600
acaaccactc ccctgggaaa cagatacatg gctcttatcc aacacagcac          650
tatcatcggg ttttctcagg tgtttgagcc acaccagaag aaacaaacgc          700
gagcttcagt ggtgattcca gtgactgggg atagtgaagg tgctacggtg          750
cagctgactc catatttttc tacttgtggc agcgactgca tccgacataa          800

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aggaacagtt gtgctctgcc cacaaacagg cgtccctttc cctctggata      850
acaacaaaag caagccggga ggctggctgc ctctcctcct gctgtctctg      900
ctggtggcca catgggtgct ggtggcaggg atctatctaa tgtggaggca      950
cgaaaggatc aagaagactt ccttttctac caccacacta ctgcccccca     1000
ttaaggttct tgtggtttac ccatctgaaa tatgtttcca tcacacaatt     1050
tgttacttca ctgaatttct tcaaaaccat tgcagaagtg aggtcatcct     1100
tgaaaagtgg cagaaaaaga aaatagcaga gatgggtcca gtgcagtggc     1150
ttgccactca aaagaaggca gcagacaaaag tcgtcttcct tctttccaat     1200
gacgtcaaca gtgtgtgcga tggtaacctgt ggcaagagcg agggcagtcc     1250
cagtgagaac tctcaagacc tcttccccct tgcctttaac cttttctgca     1300
gtgatctaag aagccagatt catctgcaca aatacgtggt ggtctacttt     1350
agagagattg atacaaaaga cgattacaat gctctcagtg tctgccccaa     1400
gtaccacctc atgaaggatg ccaactgcttt ctgtgcagaa cttctccatg     1450
tcaagcagca ggtgtcagca ggaaaaagat cacaagcctg ccacgatggc     1500
tgctgctcct tgtag                                           1515

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<210> SEQ ID NO 158

<211> LENGTH: 502

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 158

```

Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala
  1             5             10             15
Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro
          20             25             30
Ser Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu
          35             40             45
Arg Asp Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly
          50             55             60
Asp Tyr Ser Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp
          65             70             75
Ala Ser Ile Arg Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly
          80             85             90
Lys Ser Asn Phe Gln Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr
          95             100            105
Glu Ala Phe Gln Thr Gln Thr Arg Pro Ser Gly Gly Lys Trp Thr
          110            115            120
Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr Phe
          125            130            135
Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
          140            145            150
Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His
          155            160            165
Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp
          170            175            180
Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu
          185            190            195
Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu

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200					205					210				
Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	Glu	Pro
				215					220					225
His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	Thr
				230					235					240
Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro
				245					250					255
Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu
				260					265					270
Cys	Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser
				275					280					285
Lys	Pro	Gly	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val
				290					295					300
Ala	Thr	Trp	Val	Leu	Val	Ala	Gly	Ile	Tyr	Leu	Met	Trp	Arg	His
				305					310					315
Glu	Arg	Ile	Lys	Lys	Thr	Ser	Phe	Ser	Thr	Thr	Thr	Leu	Leu	Pro
				320					325					330
Pro	Ile	Lys	Val	Leu	Val	Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His
				335					340					345
His	Thr	Ile	Cys	Tyr	Phe	Thr	Glu	Phe	Leu	Gln	Asn	His	Cys	Arg
				350					355					360
Ser	Glu	Val	Ile	Leu	Glu	Lys	Trp	Gln	Lys	Lys	Lys	Ile	Ala	Glu
				365					370					375
Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	Thr	Gln	Lys	Lys	Ala	Ala	Asp
				380					385					390
Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	Val	Asn	Ser	Val	Cys	Asp
				395					400					405
Gly	Thr	Cys	Gly	Lys	Ser	Glu	Gly	Ser	Pro	Ser	Glu	Asn	Ser	Gln
				410					415					420
Asp	Leu	Phe	Pro	Leu	Ala	Phe	Asn	Leu	Phe	Cys	Ser	Asp	Leu	Arg
				425					430					435
Ser	Gln	Ile	His	Leu	His	Lys	Tyr	Val	Val	Val	Tyr	Phe	Arg	Glu
				440					445					450
Ile	Asp	Thr	Lys	Asp	Asp	Tyr	Asn	Ala	Leu	Ser	Val	Cys	Pro	Lys
				455					460					465
Tyr	His	Leu	Met	Lys	Asp	Ala	Thr	Ala	Phe	Cys	Ala	Glu	Leu	Leu
				470					475					480
His	Val	Lys	Gln	Gln	Val	Ser	Ala	Gly	Lys	Arg	Ser	Gln	Ala	Cys
				485					490					495
His	Asp	Gly	Cys	Cys	Ser	Leu								
				500										

<210> SEQ ID NO 159

<211> LENGTH: 535

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 159

agccaccagc gcaacatgac agtgaagacc ctgcatggcc cagccatggt	50
caagtacttg ctgctgtcga tattggggct tgcctttctg agtgaggcgg	100
cagctcggaa aatccccaaa gtaggacata cttttttcca aaagcctgag	150
agttgcccg cgtgtgccag aggtagtatg aagcttgaca ttggcatcat	200
caatgaaaac cagcgcggtt ccatgtcacg taacatcgag agccgctcca	250

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cctccccctg gaattacact gtcacttggg accccaaccg gtaccctcgc	300
gaagttgtac aggcccagtg taggaacttg ggctgcatca atgctcaagg	350
aaaggaagac atctccatga attccgttcc catccagcaa gagaccctgg	400
tcgtccggag gaagcaccaa ggctgctctg tttctttcca gttggagaag	450
gtgtggtga ctgttggtg cacctgcgtc acccctgtca tccaccatgt	500
gcagtaagag gtgcatatcc actcagctga agaag	535

<210> SEQ ID NO 160
 <211> LENGTH: 163
 <212> TYPE: PRT
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 160

Met Thr Val Lys Thr Leu His Gly Pro Ala Met Val Lys Tyr Leu	1	5	10	15
Leu Leu Ser Ile Leu Gly Leu Ala Phe Leu Ser Glu Ala Ala Ala	20	25	30	
Arg Lys Ile Pro Lys Val Gly His Thr Phe Phe Gln Lys Pro Glu	35	40	45	
Ser Cys Pro Pro Val Pro Gly Gly Ser Met Lys Leu Asp Ile Gly	50	55	60	
Ile Ile Asn Glu Asn Gln Arg Val Ser Met Ser Arg Asn Ile Glu	65	70	75	
Ser Arg Ser Thr Ser Pro Trp Asn Tyr Thr Val Thr Trp Asp Pro	80	85	90	
Asn Arg Tyr Pro Ser Glu Val Val Gln Ala Gln Cys Arg Asn Leu	95	100	105	
Gly Cys Ile Asn Ala Gln Gly Lys Glu Asp Ile Ser Met Asn Ser	110	115	120	
Val Pro Ile Gln Gln Glu Thr Leu Val Val Arg Arg Lys His Gln	125	130	135	
Gly Cys Ser Val Ser Phe Gln Leu Glu Lys Val Leu Val Thr Val	140	145	150	
Gly Cys Thr Cys Val Thr Pro Val Ile His His Val Gln	155	160		

<210> SEQ ID NO 161
 <211> LENGTH: 2380
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 161

acactggcca aacaaaaacg aaagcactcc gtgctggaag taggaggaga	50
gtcaggactc ccaggacaga gagtgcacaa actaccacgc acagccccct	100
ccgccccctc tggaggctga agagggattc cagccccctgc caccacaga	150
cacgggctga ctgggggtgc tgccccctt gggggggggc agcacagggc	200
ctcaggcctg ggtgccacct ggcacctaga agatgcctgt gccctggttc	250
ttgtgtcctc tggcactggg ccgaagccca gtggtccttt ctctggagag	300
gcttgtgggg cctcaggacg ctaccactg ctctccgggc ctctcctgcc	350
gcctctggga cagtacata ctctgcctgc ctggggacat cgtgcctgct	400
ccgggccccg tgctggcgcc tacgcacctg cagacagagc tggtgctgag	450

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gtgccagaag gagaccgact gtgacctctg tctgcgtgtg gctgtccact	500
tggccgtgca tgggcactgg gaagagcctg aagatgagga aaagtttgga	550
ggagcagctg actcaggggt ggagagcct aggaatgcct ctctccaggc	600
ccaagtcgtg ctctccttcc aggcctaccc tactgcccgc tgcgtcctgc	650
tggagggtgca agtgccctgct gcccttgtgc agtttggtea gtctgtgggc	700
tctgtggtat atgactgctt cgaggtgccc ctaggagtg aggtacgaat	750
ctggtcctat actcagccca ggtacgagaa ggaactcaac cacacacagc	800
agctgcctgc cctgccctgg ctcaacgtgt cagcagatgg tgacaacgtg	850
catctggttc tgaatgtctc tgaggagcag cacttcggcc tctccctgta	900
ctggaatcag gtccagggcc ccccaaaacc ccggtggcac aaaaacctga	950
ctggaccgca gatcattacc ttgaaccaca cagacctggt tccctgcctc	1000
tgtattcagg tgtggcctct ggaacctgac tccgttagga cgaacatctg	1050
ccccctcagg gaggaccccc gcgcacacca gaacctctgg caagccgccc	1100
gactgcgact gctgacctg cagagctggc tgctggacgc accgtgctcg	1150
ctgcccgcag aagcggcact gtgctggcgg gctccgggtg gggacccctg	1200
ccagccactg gtcccaccgc ttctctggga gaacgtcact gtggacaagg	1250
ttctcgagtt cccattgctg aaagccacc ctaacctctg tgttcaggtg	1300
aacagctcgg agaagctgca gctgcaggag tgcttgtggg ctgactccct	1350
ggggcctctc aaagacgatg tgctactgtt ggagacacga gggccccagg	1400
acaacagatc cctctgtgcc ttggaaccca gtggctgtac ttactaccc	1450
agcaaagcct ccacgagggc agctcgcctt ggagagtact tactacaaga	1500
cctgcagtca ggccagtgtc tgcagctatg ggacgatgac ttgggagcgc	1550
tatgggcctg ccccatggac aaatacatcc acaagcgtg ggcctcgtg	1600
tggttgccct gcctactctt tgccgctcgc ctttccctca tcctccttct	1650
caaaaaggat caccgaaaag ggtggctgag gctcttgaag caggacgtcc	1700
gctcgggggc ggccgccagg ggccgcgcgg ctctgctcct ctactcagcc	1750
gatgactcgg gtttcgagcg cctgggtggc gccctggcgt cggccctgtg	1800
ccagctgccg ctgcgcgtgg ccgtagacct gtggagccgt cgtgaactga	1850
gcgcgcaggg gcccggtgct tggtttcacg cgcagcggcg ccagaccctg	1900
caggaggcgc gcgtggtggt cttgctcttc tctcccgtg cggtggcgct	1950
gtgcagcgag tggctacagg atgggggtgc cgggcccggg gcgcacggcc	2000
cgcacgacgc cttccgcgcc tcgctcagct gogtgcgtgc cgacttcttg	2050
cagggccggg cggccggcag ctacgtgggg gcctgcttcg acaggctgct	2100
ccaccggac gccgtaccg cccttttccg caccgtgcc gtcttcacac	2150
tgccctccca actgccagac ttctggggg ccctgcagca gcctcgcgcc	2200
ccgctgtccg ggccgctcca agagagagcg gagcaagtgt cccgggccct	2250
tcagccagcc ctggatagct acttccatcc cccggggact cccgcgcgg	2300
gacgcggggg gggaccagg gcgggacctg gggcggggga cgggacttaa	2350
ataaaggcag acgctgtttt tctaaaaaaa	2380

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<210> SEQ ID NO 162
<211> LENGTH: 705
<212> TYPE: PRT
<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 162

Met Pro Val Pro Trp Phe Leu Leu Ser Leu Ala Leu Gly Arg Ser
 1             5             10            15

Pro Val Val Leu Ser Leu Glu Arg Leu Val Gly Pro Gln Asp Ala
 20            25            30

Thr His Cys Ser Pro Gly Leu Ser Cys Arg Leu Trp Asp Ser Asp
 35            40            45

Ile Leu Cys Leu Pro Gly Asp Ile Val Pro Ala Pro Gly Pro Val
 50            55            60

Leu Ala Pro Thr His Leu Gln Thr Glu Leu Val Leu Arg Cys Gln
 65            70            75

Lys Glu Thr Asp Cys Asp Leu Cys Leu Arg Val Ala Val His Leu
 80            85            90

Ala Val His Gly His Trp Glu Glu Pro Glu Asp Glu Glu Lys Phe
 95            100           105

Gly Gly Ala Ala Asp Ser Gly Val Glu Glu Pro Arg Asn Ala Ser
110            115            120

Leu Gln Ala Gln Val Val Leu Ser Phe Gln Ala Tyr Pro Thr Ala
125            130            135

Arg Cys Val Leu Leu Glu Val Gln Val Pro Ala Ala Leu Val Gln
140            145            150

Phe Gly Gln Ser Val Gly Ser Val Val Tyr Asp Cys Phe Glu Ala
155            160            165

Ala Leu Gly Ser Glu Val Arg Ile Trp Ser Tyr Thr Gln Pro Arg
170            175            180

Tyr Glu Lys Glu Leu Asn His Thr Gln Gln Leu Pro Ala Leu Pro
185            190            195

Trp Leu Asn Val Ser Ala Asp Gly Asp Asn Val His Leu Val Leu
200            205            210

Asn Val Ser Glu Glu Gln His Phe Gly Leu Ser Leu Tyr Trp Asn
215            220            225

Gln Val Gln Gly Pro Pro Lys Pro Arg Trp His Lys Asn Leu Thr
230            235            240

Gly Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys
245            250            255

Leu Cys Ile Gln Val Trp Pro Leu Glu Pro Asp Ser Val Arg Thr
260            265            270

Asn Ile Cys Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu
275            280            285

Trp Gln Ala Ala Arg Leu Arg Leu Leu Thr Leu Gln Ser Trp Leu
290            295            300

Leu Asp Ala Pro Cys Ser Leu Pro Ala Glu Ala Ala Leu Cys Trp
305            310            315

Arg Ala Pro Gly Gly Asp Pro Cys Gln Pro Leu Val Pro Pro Leu
320            325            330

Ser Trp Glu Asn Val Thr Val Asp Lys Val Leu Glu Phe Pro Leu
335            340            345

Leu Lys Gly His Pro Asn Leu Cys Val Gln Val Asn Ser Ser Glu
350            355            360

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Lys Leu Gln Leu Gln Glu Cys Leu Trp	Ala Asp Ser Leu Gly Pro
365	370 375
Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg Gly Pro Gln Asp	
380	385 390
Asn Arg Ser Leu Cys Ala Leu Glu Pro Ser Gly Cys Thr Ser Leu	
395	400 405
Pro Ser Lys Ala Ser Thr Arg Ala Ala Arg Leu Gly Glu Tyr Leu	
410	415 420
Leu Gln Asp Leu Gln Ser Gly Gln Cys Leu Gln Leu Trp Asp Asp	
425	430 435
Asp Leu Gly Ala Leu Trp Ala Cys Pro Met Asp Lys Tyr Ile His	
440	445 450
Lys Arg Trp Ala Leu Val Trp Leu Ala Cys Leu Leu Phe Ala Ala	
455	460 465
Ala Leu Ser Leu Ile Leu Leu Leu Lys Lys Asp His Ala Lys Gly	
470	475 480
Trp Leu Arg Leu Leu Lys Gln Asp Val Arg Ser Gly Ala Ala Ala	
485	490 495
Arg Gly Arg Ala Ala Leu Leu Leu Tyr Ser Ala Asp Asp Ser Gly	
500	505 510
Phe Glu Arg Leu Val Gly Ala Leu Ala Ser Ala Leu Cys Gln Leu	
515	520 525
Pro Leu Arg Val Ala Val Asp Leu Trp Ser Arg Arg Glu Leu Ser	
530	535 540
Ala Gln Gly Pro Val Ala Trp Phe His Ala Gln Arg Arg Gln Thr	
545	550 555
Leu Gln Glu Gly Gly Val Val Val Leu Leu Phe Ser Pro Gly Ala	
560	565 570
Val Ala Leu Cys Ser Glu Trp Leu Gln Asp Gly Val Ser Gly Pro	
575	580 585
Gly Ala His Gly Pro His Asp Ala Phe Arg Ala Ser Leu Ser Cys	
590	595 600
Val Leu Pro Asp Phe Leu Gln Gly Arg Ala Pro Gly Ser Tyr Val	
605	610 615
Gly Ala Cys Phe Asp Arg Leu Leu His Pro Asp Ala Val Pro Ala	
620	625 630
Leu Phe Arg Thr Val Pro Val Phe Thr Leu Pro Ser Gln Leu Pro	
635	640 645
Asp Phe Leu Gly Ala Leu Gln Gln Pro Arg Ala Pro Arg Ser Gly	
650	655 660
Arg Leu Gln Glu Arg Ala Glu Gln Val Ser Arg Ala Leu Gln Pro	
665	670 675
Ala Leu Asp Ser Tyr Phe His Pro Pro Gly Thr Pro Ala Pro Gly	
680	685 690
Arg Gly Val Gly Pro Gly Ala Gly Pro Gly Ala Gly Asp Gly Thr	
695	700 705

<210> SEQ ID NO 163

<211> LENGTH: 2478

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 163

gtcagtcgag gagccgggtc agccaccaag atgactgaca ggttcagctc

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tctgcagcac	actaccctca	agccacctga	tgtgacctgt	atctccaaag	100
tgagatcgat	tcagatgatt	gttcataccta	ccccccagcc	aatccgtgca	150
ggcgatggcc	accggctaac	cctggaagac	atcttccatg	acctgttcta	200
ccacttagag	ctccagggtca	accgcaccta	ccaaatgcac	cttggaggga	250
agcagagaga	atatgagttc	ttcggcctga	cccctgacac	agagttcctt	300
ggcaccatca	tgatttgcgt	tcccacctgg	gccaaggaga	gtgcccccta	350
catgtgccga	gtgaagacac	tgccagaccg	gacatggacc	tactccttct	400
ccggagcctt	cctgtttctcc	atgggcttcc	tcgtcgcagt	actctgctac	450
ctgagctaca	gatatgtcac	caagccgcct	gcacctcca	actccctgaa	500
cgtccagcga	gtcctgactt	tccagccgct	gcgcttcac	caggagcacg	550
tcctgatccc	tgtctttgac	ctcagcggcc	ccagcagtct	ggcccagcct	600
gtccagtact	cccagatcag	ggtgtctgga	cccagggagc	ccgcaggagc	650
tccacagcgg	catagcctgt	ccgagatcac	ctacttaggg	cagccagaca	700
tctccatcct	ccagccctcc	aacgtgccac	ctccccagat	cctctcccca	750
ctgtcctatg	ccccaaacgc	tgccctgag	gtcgggcccc	catcctatgc	800
acctcaggtg	acccccgaag	ctcaattccc	attctacgcc	ccacaggcca	850
tctctaaggt	ccagccttcc	tcctatgccc	ctcaagccac	tccggacagc	900
tggcctccct	cctatggggg	atgcatggaa	ggttctggca	aagactcccc	950
cactgggaca	ctttctagtc	ctaaacacct	taggcctaaa	ggtcagcttc	1000
agaaagagcc	accagctgga	agctgcatgt	taggtggcct	ttctctgcag	1050
gaggtgacct	ccttggtctat	ggaggaatcc	caagaagcaa	aatcattgca	1100
ccagcccctg	gggatttgca	cagacagaac	atctgaccca	aatgtgctac	1150
acagtgggga	ggaagggaca	ccacagtacc	taaagggcca	gctccccctc	1200
ctctcctcag	tccagatcga	gggccacccc	atgtccctcc	ctttgcaacc	1250
tccttccggt	ccatgttccc	cctcggacca	aggtccaagt	ccctggggcc	1300
tgtctggagtc	ccttgtgtgt	cccaaggatg	aagccaagag	cccagcccct	1350
gagacctcag	acctggagca	gccacagaa	ctggattctc	ttttcagagg	1400
cctggccctg	actgtgcagt	gggagtcctg	aggggaatgg	gaaaggcttg	1450
gtgtctcctc	cctgtcccta	cccagtgcca	catccttggc	tgtcaatccc	1500
atgcctgccc	atgccacaca	ctctgcgac	tggcctcaga	cgggtgcctt	1550
tgagagaagc	agagggagtg	gcatgcaggg	cccctgcat	gggtgcgctc	1600
ctcaccggaa	caaagcagca	tgataaggac	tgacgcgggg	gagctctggg	1650
gagcagcttg	tgtagacaag	cgcgtgctcg	ctgagccctg	caaggcagaa	1700
atgacagtgc	aaggaggaaa	tgcagggaaa	ctcccgaggt	ccagagcccc	1750
acctcctaac	accatggatt	caaagtgtct	agggaatttg	cctctccttg	1800
ccccattcct	ggccagtttc	acaatctagc	tcgacagagc	atgaggcccc	1850
tgcctcttct	gtcattgttc	aaagtgggga	agagagcctg	gaaaagaacc	1900
aggcctggaa	aagaaccaga	aggaggctgg	gcagaaccag	aacaacctgc	1950
acttctgcca	aggccagggc	cagcaggacg	gcaggactct	agggaggggt	2000

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gtggcctgca gctcattccc agccagggca actgcctgac gttgcacgat      2050
ttcagcttca ttctctgat agaacaaagc gaaatgcagg tccaccaggg      2100
agggagacac acaagccttt tctgcaggca ggagtttcag accctatcct      2150
gagaatgggg ttgaaagga aggtgagggc tgtggcccct ggacgggtac      2200
aataacacac tgtactgatg tcacaacttt gcaagctctg ccttgggttc      2250
agcccatctg ggctcaaatt ccagcctcac cactcacaag ctgtgtgact      2300
tcaaacaagt gaaatcagtg ccagaaacct cggtttcctc atctgtaatg      2350
tggggatcat aacacctacc tcatggagtt gtggtgaaga tgaatgaag      2400
tcatgtcttt aaagtctta atagtgcctg gtacatgggc agtgcccaat      2450
aaacggtagc tatttaaaaa aaaaaaaa      2478

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<210> SEQ ID NO 164

<211> LENGTH: 574

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 164

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Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala
 1             5             10             15
His Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe
20            25            30
Gln Ser Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro
35            40            45
Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr
50            55            60
Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr
65            70            75
Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn Leu Thr Glu
80            85            90
Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly Arg Ser
95           100           105
Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr Thr
110          115          120
Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile
125          130          135
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp
140          145          150
Gly His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr
155          160          165
His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly
170          175          180
Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr
185          190          195
Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys
200          205          210
Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
215          220          225
Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
230          235          240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr
245          250          255

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Lys Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu
 260 265 270
 Thr Phe Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro
 275 280 285
 Val Phe Asp Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln
 290 295 300
 Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala
 305 310 315
 Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro
 320 325 330
 Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro Gln Ile
 335 340 345
 Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val Gly
 350 355 360
 Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro
 365 370 375
 Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr
 380 385 390
 Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val
 395 400 405
 Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser
 410 415 420
 Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro
 425 430 435
 Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val
 440 445 450
 Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu His
 455 460 465
 Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 470 475 480
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln
 485 490 495
 Leu Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser
 500 505 510
 Leu Pro Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln
 515 520 525
 Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys
 530 535 540
 Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln
 545 550 555
 Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala Leu Thr Val
 560 565 570
 Gln Trp Glu Ser

<210> SEQ ID NO 165

<211> LENGTH: 1060

<212> TYPE: DNA

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 165

tggcctactg gaaaaaaaaa aaaaaaaaaa aaaagtcacc cgggcccgcg	50
gtggccacaa catggctgcg gcgccggggc tgctcttctg gctgttcgtg	100
ctggggggcgc tctggtgggt cccggggccag tcggatctca gccacggacg	150

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gcgtttctcg gacctcaaag tgtgcgggga cgaagagtgc agcatgttaa	200
tgtaccgtgg gaaagctctt gaagacttca cgggccctga ttgtcgtttt	250
gtgaatttta aaaaagggtga cgatgtatat gtctactaca aactggcagg	300
gggatccctt gaactttggg ctggaagtgt tgaacacagt tttggatatt	350
ttccaaaaga ttgatcaag gtacttcata aatacacgga agaagagcta	400
catattccag cagatgagac agactttgtc tgctttgaag gaggaagaga	450
tgattttaat agttataatg tagaagagct tttaggatct ttggaactgg	500
aggactctgt acctgaagag tcgaagaaag ctgaagaagt ttctcagcac	550
agagagaaat ctccctgagga gtctcggggg cgtgaacttg acctgtgcc	600
tgagcccag gcatcagag ctgattcaga ggatggagaa ggtgctttct	650
cagagagcac cgaggggctg cagggacagc cctcagctca ggagagccac	700
cctcacacca gcggtcctgc ggctaacgct cagggagtgc agtcttcgtt	750
ggacactttt gaagaaattc tgcacgataa attgaaagtg ccgggaagcg	800
aaagcagaac tggcaatagt tctcctgcct cggtgagcg ggagaagaca	850
gatgcttaca aagtcctgaa aacagaaatg agtcagagag gaagtggaca	900
gtgcgttatt cattacagca aaggatttcg ttggcatcaa aatctaagtt	950
tgttttacaa agattgtttt tagtactaag ctgccttggc agtttgcat	1000
tttgagccaa acaaaaatat attattttcc cttctaagta aaaaaaaaaa	1050
aaaaaaaaaa	1060

<210> SEQ ID NO 166

<211> LENGTH: 303

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 166

Met Ala Ala Ala Pro Gly Leu Leu Phe Trp Leu Phe Val Leu Gly	
1 5 10 15	
Ala Leu Trp Trp Val Pro Gly Gln Ser Asp Leu Ser His Gly Arg	
20 25 30	
Arg Phe Ser Asp Leu Lys Val Cys Gly Asp Glu Glu Cys Ser Met	
35 40 45	
Leu Met Tyr Arg Gly Lys Ala Leu Glu Asp Phe Thr Gly Pro Asp	
50 55 60	
Cys Arg Phe Val Asn Phe Lys Lys Gly Asp Asp Val Tyr Val Tyr	
65 70 75	
Tyr Lys Leu Ala Gly Gly Ser Leu Glu Leu Trp Ala Gly Ser Val	
80 85 90	
Glu His Ser Phe Gly Tyr Phe Pro Lys Asp Leu Ile Lys Val Leu	
95 100 105	
His Lys Tyr Thr Glu Glu Glu Leu His Ile Pro Ala Asp Glu Thr	
110 115 120	
Asp Phe Val Cys Phe Glu Gly Gly Arg Asp Asp Phe Asn Ser Tyr	
125 130 135	
Asn Val Glu Glu Leu Leu Gly Ser Leu Glu Leu Glu Asp Ser Val	
140 145 150	
Pro Glu Glu Ser Lys Lys Ala Glu Glu Val Ser Gln His Arg Glu	
155 160 165	

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Lys Ser Pro Glu Glu Ser Arg Gly Arg Glu Leu Asp Pro Val Pro
 170 175 180
 Glu Pro Glu Ala Phe Arg Ala Asp Ser Glu Asp Gly Glu Gly Ala
 185 190 195
 Phe Ser Glu Ser Thr Glu Gly Leu Gln Gly Gln Pro Ser Ala Gln
 200 205 210
 Glu Ser His Pro His Thr Ser Gly Pro Ala Ala Asn Ala Gln Gly
 215 220 225
 Val Gln Ser Ser Leu Asp Thr Phe Glu Glu Ile Leu His Asp Lys
 230 235 240
 Leu Lys Val Pro Gly Ser Glu Ser Arg Thr Gly Asn Ser Ser Pro
 245 250 255
 Ala Ser Val Glu Arg Glu Lys Thr Asp Ala Tyr Lys Val Leu Lys
 260 265 270
 Thr Glu Met Ser Gln Arg Gly Ser Gly Gln Cys Val Ile His Tyr
 275 280 285
 Ser Lys Gly Phe Arg Trp His Gln Asn Leu Ser Leu Phe Tyr Lys
 290 295 300
 Asp Cys Phe

<210> SEQ ID NO 167
 <211> LENGTH: 2570
 <212> TYPE: DNA
 <213> ORGANISM: Homo Sapien

<400> SEQUENCE: 167

ccaggaccag ggcgcaccgg ctcagcctct cacttgctcag aggccgggga	50
agagaagcaa agcgcaacgg tgtgtgtccaa gccgggggctt ctgcttcgcc	100
tctaggacat acacggggacc ccctaacttc agtcccccaa acgcgcaccc	150
tcgaagtctt gaactccagc cccgcacatc cacgcgcggc acaggcgcgg	200
caggcggcag gtcccggccg aaggcgatgc gcgcaggggg tcgggcagct	250
gggctcgggc ggcgggagta gggcccggca gggaggcagg gaggctgcat	300
attcagagtc gcgggctgcg ccctgggcag aggcgcgcct cgctccacgc	350
aacacctgct gctgccaccg cgccgcgatg agccgcgtgg tctcgctgct	400
gctgggcgcc gcgctgctct gcggccacgg agccttctgc cgccgcgtgg	450
tcagcggcca aaaggtgtgt ttgtgtgact tcaagcatcc ctgctacaaa	500
atggcctact tccatgaact gtccagccga gtgagctttc aggaggcacg	550
cctggcttgt gagagtgagg gaggagtcct cctcagcctt gagaatgaag	600
cagaacagaa gttaatatag agcatgttgc aaaacctgac aaaacccggg	650
acaggggattt ctgatgtgta tttctggata gggctttgga ggaatggaga	700
tgggcaaaca tctggtgcct gccagatct ctaccagtgg tctgatggaa	750
gcaattccca gtaccgaaac tggtaacacag atgaaccttc ctgcggaagt	800
gaaaagtgtg ttgtgatgta tcaccaacca actgccaatc ctggccttgg	850
gggtccctac ctttaccagt ggaatgatga cagggtgaac atgaagcaca	900
attatatttg caagtatgaa ccagagatta atccaacagc ccctgtagaa	950
aagccttata ttacaaatca accaggagac acccatcaga atgtggttgt	1000
tactgaagca ggtataattc ccaatcctaat ttatgttgtt ataccaacaa	1050

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taccctctgct cttactgata ctggttgctt ttggaacctg ttgtttccag	1100
atgctgcata aaagtaaagg aagaacaaaa actagtccaa accagtctac	1150
actgtggatt tcaaagagta ccagaaaaga aagtggcatg gaagtataat	1200
aactcattga cttggttcca gaattttgta attctggatc tgtataagga	1250
atggcatcag aacaatagct tggaaatggct tgaaatcaca aaggatctgc	1300
aagatgaact gtaagctccc ccttgaggca aatattaaag taatttttat	1350
atgtctatta tttcatttaa agaatatgct gtgctaataa tggagtgaga	1400
catgcttatt ttgctaaagg atgcacccaa acttcaaact tcaagcaaat	1450
gaaatggaca atgcagataa agttgttatc aacacgtcgg gagtatgtgt	1500
gttagaagca attcctttta tttctttcac ctttcataag ttgttatcta	1550
gtcaatgtaa tgtatatgtt attgaaattt acagtgtgca aaagtatttt	1600
acctttgcat aagtgtttga taaaaatgaa ctgttctaatt atttattttt	1650
atggcatctc atttttcaat acatgctctt ttgattaaag aaacttatta	1700
ctgttgtcaa ctgaattcac acacacacaa atatagtacc atagaaaaag	1750
tttgttttct cgaaataatt catctttcag cttctctgct tttggtcaat	1800
gtctaggaaa tctcttcaga aataagaagc tatttcatta agtgtgatat	1850
aaacctctc aaacatttta cttagaggca aggattgtct aatttcaatt	1900
gtgcaagaca tgtgccttat aattattttt agcttaaaat taaacagatt	1950
ttgtaataat gtaactttgt taataggtgc ataaacacta atgcagtcga	2000
tttgaacaaa agaagtgaca tacacaatat aaatcatatg tcttcacacg	2050
ttgcctatat aatgagaagc agctctctga gggttctgaa atcaatgtgg	2100
tccctctctt gcccaactaaa caaagatggg ttgtcggggg ttgggattga	2150
cactggaggc agatagttgc aaagttagtc taaggtttcc ctgctgttat	2200
ttagcctctg actatattag tatacaaaga ggtcatgtgg ttgagaccag	2250
gtgaatagtc actatcagtg tggagacaag cacagcacac agacatttta	2300
ggaaggaaa gaactacgaa atcgtgtgaa aatgggttgg aacccatcag	2350
tgatcgcata ttcattgatg agggtttgct tgagatagaa aatgggtggc	2400
cctttctgtc ttatctccta gtttcttcaa tgcttacgcc ttgttcttct	2450
caagagaaa ttgtaactct ctggtcttca tatgtccctg tgctcctttt	2500
aaccaaataa agagttcttg tttctggggg aaaaaaaaaa aaaaaaaaaa	2550
aaaaaaaaa aaaaaaaaaa	2570

<210> SEQ ID NO 168

<211> LENGTH: 273

<212> TYPE: PRT

<213> ORGANISM: Homo Sapien

<400> SEQUENCE: 168

Met	Ser	Arg	Val	Val	Ser	Leu	Leu	Leu	Gly	Ala	Ala	Leu	Leu	Cys
1				5					10					15

Gly	His	Gly	Ala	Phe	Cys	Arg	Arg	Val	Val	Ser	Gly	Gln	Lys	Val
				20					25					30

Cys	Phe	Ala	Asp	Phe	Lys	His	Pro	Cys	Tyr	Lys	Met	Ala	Tyr	Phe
				35				40						45

-continued

His	Glu	Leu	Ser	Ser	Arg	Val	Ser	Phe	Gln	Glu	Ala	Arg	Leu	Ala
				50					55					60
Cys	Glu	Ser	Glu	Gly	Gly	Val	Leu	Leu	Ser	Leu	Glu	Asn	Glu	Ala
				65					70					75
Glu	Gln	Lys	Leu	Ile	Glu	Ser	Met	Leu	Gln	Asn	Leu	Thr	Lys	Pro
				80					85					90
Gly	Thr	Gly	Ile	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Trp	Arg
				95					100					105
Asn	Gly	Asp	Gly	Gln	Thr	Ser	Gly	Ala	Cys	Pro	Asp	Leu	Tyr	Gln
				110					115					120
Trp	Ser	Asp	Gly	Ser	Asn	Ser	Gln	Tyr	Arg	Asn	Trp	Tyr	Thr	Asp
				125					130					135
Glu	Pro	Ser	Cys	Gly	Ser	Glu	Lys	Cys	Val	Val	Met	Tyr	His	Gln
				140					145					150
Pro	Thr	Ala	Asn	Pro	Gly	Leu	Gly	Gly	Pro	Tyr	Leu	Tyr	Gln	Trp
				155					160					165
Asn	Asp	Asp	Arg	Cys	Asn	Met	Lys	His	Asn	Tyr	Ile	Cys	Lys	Tyr
				170					175					180
Glu	Pro	Glu	Ile	Asn	Pro	Thr	Ala	Pro	Val	Glu	Lys	Pro	Tyr	Leu
				185					190					195
Thr	Asn	Gln	Pro	Gly	Asp	Thr	His	Gln	Asn	Val	Val	Val	Thr	Glu
				200					205					210
Ala	Gly	Ile	Ile	Pro	Asn	Leu	Ile	Tyr	Val	Val	Ile	Pro	Thr	Ile
				215					220					225
Pro	Leu	Leu	Leu	Leu	Ile	Leu	Val	Ala	Phe	Gly	Thr	Cys	Cys	Phe
				230					235					240
Gln	Met	Leu	His	Lys	Ser	Lys	Gly	Arg	Thr	Lys	Thr	Ser	Pro	Asn
				245					250					255
Gln	Ser	Thr	Leu	Trp	Ile	Ser	Lys	Ser	Thr	Arg	Lys	Glu	Ser	Gly
				260					265					270

Met Glu Val

<210> SEQ ID NO 169
 <211> LENGTH: 43
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
 <400> SEQUENCE: 169

tgtaaaacga cggccagtta aatagacctg caattattaa tct

43

<210> SEQ ID NO 170
 <211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
 <400> SEQUENCE: 170

caggaaacag ctatgaccac ctgcacacct gcaaatccat t

41

455

The invention claimed is:

1. An isolated polypeptide comprising:

(a) the amino acid sequence of the polypeptide of SEQ ID NO:28;

(b) the amino acid sequence of the polypeptide of SEQ ID NO:28 lacking its associated signal peptide; or

(c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209952.

2. The isolated polypeptide of claim 1 comprising the amino acid sequence of the polypeptide of SEQ ID NO:28.

3. The isolated polypeptide of claim 1 comprising the amino acid sequence of the polypeptide of SEQ ID NO:28, lacking its associated signal peptide.

456

4. The isolated polypeptide of claim 1 comprising the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209952.

5. A chimeric polypeptide comprising a polypeptide according to claim 1 fused to a heterologous polypeptide.

6. The chimeric polypeptide of claim 5, wherein said heterologous polypeptide is a tag polypeptide or an Fc region of an immunoglobulin.

* * * * *